

Result No.	Query	Score	Match Length	DB ID	Description
1	A_Geneseq_16Dpac04:*	89.6	44	RAY18305	Aay18305 Human fac
2	Geneseqp1980s:*	89.6	44	AAB36395	Aab36395 Human fac
3	Geneseqp1990s:*	89.6	44	ADD50096	Add50096 Human vit
4	Geneseqp2000s:*	89.6	44	ADQ269602	Adq269602 Human fac
5	Geneseqp2001s:*	89.6	401	AAB84870	Aab84870 Mutant bl
6	Geneseqp2002s:*	89.6	401	AAB84871	Aab84871 Mutant bl
7	Geneseqp2003ab:*	89.6	406	AAR35764	Aar35764 Factor VI
8	Geneseqp2004s:*	89.6	406	AAW14510	Aaw14510 Modified
9				Aaw14509	Aaw14509 Modified
10				Aau7745	Aau7745 Human fac
11				Aab84867	Aab84867 Mutant bl
12				Aab84868	Aab84868 Mutant bl
13				Aab84869	Aab84869 Mutant bl
14				Aab84866	Aab84866 Wild-type
15				Aams5183	Aams5183 Human FVI
16				Aam52182	Aam52182 Mammalian
17				Aam52182	Aam52182 Human FVI
18				Aams52186	Aams52186 Human FVI
19				Aams52171	Aams52171 Human FVI
20				Aams52187	Aams52187 Human FVI
21				Aams52181	Aams52181 Human FVI
22				Aams52185	Aams52185 Human FVI
23				Aams52184	Aams52184 Human FVI
24				Aams52182	Aams52182 Human FVI
25				Aau77196	Aau77196 Human coa

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:19:07 ; Search time 70 Seconds
(without alignments)

Title: US-10-031-005-3

Perfect score: 192

Sequence: 1 ANAFLXXLRPGSILXRCKXX.XXARXIFKDAARTKLFWIY 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : A_Geneseq_16Dpac04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003ab:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
1	AAY18305	89.6	44	RAY18305	Aay18305 Human fac
2	AAB36395	89.6	44	AAB36395	Aab36395 Human fac
3	ADD50096	89.6	44	ADD50096	Add50096 Human vit
4	ADQ269602	89.6	44	ADQ269602	Adq269602 Human fac
5	AAB84870	89.6	401	AAB84870	Aab84870 Mutant bl
6	AAB84871	89.6	401	AAB84871	Aab84871 Mutant bl
7	AAR35764	89.6	406	AAR35764	Aar35764 Factor VI
8	AAW14510	89.6	406	AAW14510	Aaw14510 Modified
9	Aaw14509	89.6	406	Aaw14509	Aaw14509 Modified
10	Aau7745	89.6	406	Aau7745	Aau7745 Human fac
11	Aab84867	89.6	406	Aab84867	Aab84867 Mutant bl
12	Aab84868	89.6	406	Aab84868	Aab84868 Mutant bl
13	Aab84869	89.6	406	Aab84869	Aab84869 Mutant bl
14	Aab84866	89.6	406	Aab84866	Aab84866 Wild-type
15	Aams5183	89.6	406	Aams5183	Aams5183 Human FVI
16	Aam52182	89.6	406	Aam52182	Aam52182 Mammalian
17	Aams52186	89.6	406	Aams52186	Aams52186 Human FVI
18	Aams52171	89.6	406	Aams52171	Aams52171 Human FVI
19	Aams52187	89.6	406	Aams52187	Aams52187 Human FVI
20	Aams52181	89.6	406	Aams52181	Aams52181 Human FVI
21	Aams52185	89.6	406	Aams52185	Aams52185 Human FVI
22	Aams52184	89.6	406	Aams52184	Aams52184 Human FVI
23	Aams52182	89.6	406	Aams52182	Aams52182 Human FVI
24	Aau77196	89.6	406	Aau77196	Aau77196 Human coa
25	Aau77191	89.6	406	Aau77191	Aau77191 Human coa

ALIGNMENTS

RESULT 1
ID AAY18305 standard; peptide; 44 AA.
XX
AC AAY18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Misc-difference 1 .44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT
FT
XX
PN WO9920767-A1.

Location/Qualifiers
1 .44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
Key
Misc-difference 1 .44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
FT
FT
FT
XX
XX
PD 29-APR-1999.
XX
PP 20-OCT-1998;
XX
PR 23-OCT-1997;
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Nelsetuen GL;
XX
DR WPI ; 1999-288309/24.
XX
CC 9BNO-US022152.
XX
PR 97US-00955636.
XX
PA
XX
XX
XX
PS Disclosure; Page 15: 86pp; English.
XX
XX
CC This sequence is the Factor VII GLA (gamma-carboxyglutamic acid) domain.
CC The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances CC membrane binding of the modified polypeptide as compared to the native CC polypeptide. The polypeptide is used to treat a clotting disorder by CC decreasing or increasing clot formation. Modification of the GLA domain CC results in a protein which has enhanced membrane binding affinity as CC compared to the native protein
XX
SQ Sequence 44 AA;

Query Match Similarity 89.6%; Score 172; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1.2e-21; Indels 0; Gaps 0;
 Matches 44; Conservative 0; Mismatches 0; Delins 0;

Qy 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44
 Db 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44

RESULT 2
 AAB6395 Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 ID AAB6395 standard; peptide; 44 AA.
 XX DE Human vitamin K-dependent protein #2.
 AC KW Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
 XX GLA domain; membrane binding affinity; clot formation; haemostatic; anticoagulant;
 XX clotting disorder; site directed mutagenesis; thrombolytic.

XX OS Homo sapiens.
 XX PN US2003100506-A1.
 XX PD 29-MAY-2003.
 XX PP 18-NOV-2002; 2002US-00298330.

XX KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 KW factor X; prothrombin; enhanced membrane binding affinity;
 KW clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
 KW clotting disorder; haemophilia A; haemophilia B; liver disease.
 XX OS Homo sapiens.
 XX WO20066753-A2.
 XX PN
 XX PD 09-NOV-2000.
 XX PF 28-APR-2000; 2000WO-US011416.

XX PR 29-APR-1999; 99US-00302239.
 XX (MINU) UNIV MINNESOTA.
 PA XX Disclosure: Page 12; 81pp; English.
 PI XX Sequence 44 AA;

DR 2001-007226/01.

XX Novel vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified gamma-carboxy glutamic acid domain that enhances membrane binding affinity.
 XX Disclosure: Page 12; 81pp; English.
 CC The present invention describes a vitamin K-dependent polypeptide (I) comprising a modified gamma-carboxy glutamic acid (GLA) domain having at least one amino acid substitution, that enhances membrane binding affinity and the activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide and inhibits clot formation. (I) can have thrombolytic and haemostatic activities, and can be used as an inhibitor of clot formation. (I) is useful for decreasing clot formation in a mammal, a factor VII or factor IX containing a modified GLA domain is useful for increasing clot formation and for treating a bleeding disorder, including thrombosis and clotting disorders such as haemophilia A, haemophilia B and liver disease. The present sequence represents a wild type human factor VII GLA domain sequence, given in the exemplification of the present invention
 XX Sequence 44 AA;

Qy 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44
 Db 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44

RESULT 3
 ADD50096 Standard; protein; 44 AA.
 ID ADD50096
 XX AC ADD50096;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human vitamin K-dependent protein #2.
 XX KW Human; vitamin K-dependent protein; gamma-carboxyglutamic acid domain;
 KW GLA domain; membrane binding affinity; clot formation; haemostatic; anticoagulant;
 KW clotting disorder; site directed mutagenesis; thrombolytic.

XX OS Homo sapiens.
 XX PN US2003100506-A1.
 XX PD 29-MAY-2003.
 XX PP 18-NOV-2002; 2002US-00298330.

XX PR 23-OCT-1997; 97US-00955636.
 PR 29-APR-1999; 99US-00302239.
 PR 03-FEB-2000; 2000US-00497591.

XX PA (NELS/) NELSESTUEN G L.

XX PI Nelsestuen GL;
 XX DR WPI; 2003-60646/57.
 XX PT New vitamin K-dependent polypeptide for modulating clot formation in mammals comprises a modified gamma-carboxyglutamic acid domain that enhances membrane binding affinity and activity of the polypeptide.

XX PS Example 5; SBQ ID NO 3; Sipp; English.
 XX The invention relates to a vitamin K-dependent polypeptide comprising a modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane binding affinity and activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide, where the modified GLA domain comprises a glutamic acid residue at position 34. The polypeptide is useful in modulating clot formation in mammals. Or in treating certain types of haemophilia or clotting disorders. The membrane binding affinity of polypeptides is increased by site directed mutagenesis in the GLA domain. This sequence represents a vitamin K-dependent protein of the invention.
 XX SQ Sequence 44 AA;

CC The invention relates to a vitamin K-dependent polypeptide comprising a modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane binding affinity and activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide, where the modified GLA domain comprises a glutamic acid residue at position 34. The polypeptide is useful in modulating clot formation in mammals. Or in treating certain types of haemophilia or clotting disorders. The membrane binding affinity of polypeptides is increased by site directed mutagenesis in the GLA domain. This sequence represents a vitamin K-dependent protein of the invention.
 XX Query Match Similarity 89.6%; Score 172; DB 7; Length 44;
 CC Best Local Similarity 100.0%; Pred. No. 1.2e-21; Indels 0; Gaps 0;
 CC Matches 44; Conservative 0; Mismatches 0; Delins 0;
 CC Matches 44; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44
 Db 1 ANAFLXXLRPGSLXRXCXQQCSFXXARYKIFKDAVRTKLFWIISY 44

RESULT 4
 ADD26902 Standard; protein; 44 AA.
 ID ADD26902
 XX AC ADD26902;
 XX DT 26-AUG-2004 (first entry)
 XX DE Human factor VII Gamma-carboxyglutamic acid (GLA) domain.
 XX KW Human; clot formation; protein C; activated protein C; APC;
 KW gamma-carboxyglutamic acid domain; GLA domain; vitamin K-dependent;

KW aspirin; heparin; haemophilic disorder; haemostatic;	
KW anticoagulant; Factor VII.	
XX Homo sapiens.	
OS XX	FT PT XX
Key Location/Qualifiers	PT XX
PH Misc-difference 1..44	PN JP2001061479-A.
FT /label= OTHER	XX
FT /note= "OTHER= All Xaa residues are glutamic acid or	PD 13-MAR-2001.
FT gamma carboxyglutamic acid"	XX
FT XX	PF 24-AUG-1999;
PN 08-JUN-2004.	XX
XX	PR 24-AUG-1999;
PD 08-JUN-2004.	XX
XX	XX (KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.
XX	DR N-PSDB; AAH19463.
XX	DR WPI; 2001-310677/33.
XX	XX Mutant of blood coagulant factor VII, used for substitution therapy in
XX	PT the treatment of hemophilia.
PR 23-OCT-1997; 97US-00955536.	XX
PR 29-APR-1999; 99US-00302239.	XX
XX	PS Claim 14; Page 20-21; 29pp; Japanese.
PA (MINU) UNIV MINNESOTA.	XX
XX	CC The present invention relates to mutants of blood coagulant factor VII (FVII). The present
PI Nelsestuen GL;	CC sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX	CC agent for the substitution therapy of haemophilia inhibitor patients
DR 2004-429803/40.	XX
XX	SQ Sequence 401 AA;
PT Decreasing clot formation by administering an anticoagulant agent, and a	Query Match Score 172; DB 4; Length 401;
PT protein C or activated protein C polypeptide having a modified GLA	Best Local Similarity 77.3%; Pred. No. 1.2e-20;
PT domain, useful for treating hemophilic disorders in mammals.	Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
PS Example 5; SEQ ID NO 3; 41pp; English.	Qy 1 ANAFLXXLRLPSSLXRXCCKXXQCSPEXXARXIFKDAXRTKLFWIISY 44
XX	Db 1 ANAFLELRLPSSLERECKEEQCSPEEAREIFKDAAERTKLFWIISY 44
PT The invention relates to a method of decreasing clot formation comprising	RESULT 6
PT administering to a patient an anticoagulant agent and a protein C or	ID AAB84871 standard; protein; 401 AA.
PT activated protein C (APC) polypeptide comprising a modified gamma-	XX
CC carboxyglutamic acid (GLA) domain with two, three, four or five amino	ID AAB84871 standard; protein; 401 AA.
CC acid substitutions. The invention also relates to vitamin K-dependent	XX
CC nucleic acids, polypeptides, host cells, vectors and antibodies used in	ID AAB84871 standard; protein; 401 AA.
CC the methods of the invention. The anticoagulant agent is aspirin,	XX
CC warfarin or heparin, preferably aspirin. The methods and compositions of	ID AAB84871 standard; protein; 401 AA.
CC the present invention are useful for modulating clot formation for	XX
CC treating haemophilic disorders in mammals. This sequence represents the	ID AAB84871 standard; protein; 401 AA.
CC human factor VII GLA domain, used in the method of the invention.	XX
XX	DT 31-JUL-2001 (first entry)
SQ Sequence 44 AA;	XX
Query Match Score 172; DB 8; Length 44;	DB Mutant blood coagulant factor VII (FVII-39).
Best Local Similarity 100.0%; Pred. No. 1.2e-21;	XX
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
Qy 1 ANAFLXXLRLPSSLXRXCCKXXQCSPEXXARXIFKDAXRTKLFWIISY 44	KW mutant; mutein.
Db 1 ANAFLXLRLPSSLERECKEEQCSPEEAREIFKDAAERTKLFWIISY 44	XX
XX	OS Homo sapiens.
XX	OS Synthetic.
XX	PH Key Location/Qualifiers
XX	PT Misc-difference 235..239
XX	PT /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-
XX	PT Arg-Lys-Thr-Leu"
AC AAB84870;	XX
XX	PS DR N-PSDB; AAH19464.
AC AAB84870;	XX
XX	PS DR WPI; 2001-310677/33.
DT 31-JUL-2001 (first entry)	XX
XX	DE PD 13-MAR-2001.
DE Mutant blood coagulant factor VII (FVII-31).	XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;	PF 24-AUG-1999;
KW mutant; mutein.	XX
XX	PR 24-AUG-1999;
OS Homo sapiens.	XX
OS Synthetic.	PA (KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.
XX	DR N-PSDB; AAH19464.
PH Key Location/Qualifiers	XX
PT Misc-difference 311..317	DR WPI; 2001-310677/33.

XX Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia.
XX Claim 16: Page 23-24; 29pp; Japanese.

XX The present invention relates to mutants of blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match Score 172; DB 4; Length 401;
Best Local Similarity 77.3%; Pred. No. 1.2e-20; Indels 0; Gaps 0;
Matches 34; Conservative 0; Nismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRXCXXQCSFXKXARIFKDAKRTKLFWIISY 44
Db 1 ANAFDBELRPGSLERECKEBQCSFEEAREIFKDAERTKLFWIISY 44

RESULT 7
ID AAR15764 standard; protein; 406 AA.

AC AAR15764;
XX DT 25-MAR-2003 (revised)
XX DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

XX PC; protein C; IX; Factor IX; X; Factor X; PT; Prothrombin; VII;
KW Factor VII; CR; chymotrypsinogen; SP; serine protease; binding; exosite;
KW catalytic activity.

XX OS Homo sapiens.

XX Key Location/Qualifiers
FT Region 1..152
FT /note= "Factor VII light chain"
FT Region 153..406
FT /note= "Factor VII heavy chain"
FT Peptide 245..266
FT /note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 29-304, 290-304, 290-310, 374-388 and 400-414 but not with fragment 245-266"
FT Peptide 289..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 290..310
FT /note= "exosite 2"
FT Peptide 290..310
FT /note= "pref. PC polypeptide; claim 2, page 136"
FT Peptide 290..304
FT /note= "pref. PC polypeptide; claim 4, page 137"
FT Peptide 374..388
FT /note= "exosite 1"
FT Peptide 374..388
FT /note= "pref. PC polypeptide; claim 2, page 136"
XX WO9309804-A1.
XX PD 27-MAY-1993.
XX PP 18-NOV-1992; 92N0-US010242.
XX PR 18-NOV-1991; 91US-00793989.
XX PA (SCHI) SCRIPPS RES INST.
XX Griffin JH, Nestor RM;
PI

DR WPI; 1993-182244/22.
XX Serine protease derived-polypeptide(s) and anti-peptide antibodies - for PT inhibiting coagulation and assaying for the presence of serine protease in fluid samples.
XX Disclosure: Page 133-135; 14pp; English.
CC The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. CC when admin. to give an intravascular blood concn. of 0.1-100 (pred. 0.5- CC 10) microm. NB: Sequences correspond to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the CC sequence listing. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 406 AA;
Query Match Score 172; DB 2; Length 406;
Best Local Similarity 77.3%; Pred. No. 1.e-20;
Matches 34; Conservative 0; Nismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRXCXXQCSFXKXARIFKDAKRTKLFWIISY 44
Db 1 ANAFDBELRPGSLERECKEBQCSFEEAREIFKDAERTKLFWIISY 44

RESULT 8
ID AAW14510 standard; protein; 406 AA.
XX AC AAW14510;
XX DT 25-MAR-2003 (revised)
XX DT 14-MAY-1997 (first entry)

DE Modified blood coagulation Factor VII (R315S).

XX Blood coagulation; factor 7; mutein; mutation; modification;
KW thrombocytopenia; von Willebrand's disease; plasma substitute.
XX Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
FT Modified-site 6
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 7
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 14
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 16
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Disulfide-bond 17..22
FT Modified-site 19
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 20
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 25
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 26
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Modified-site 29
FT /label= OTHER
FT /note= "gamma-carboxyglutamic acid"
FT Cleavage-site 32..33

FT Cleavage-site /note= "proteolytic site"
 FT 44 .45
 FT /note= "proteolytic site"
 FT 50 .61
 FT Disulfide-bond 55 .70
 FT Modified-site 63
 FT /label= OTHER
 FT Disulfide-bond 72 .81
 FT Disulfide-bond 91 .102
 FT Disulfide-bond 98 .112
 FT Disulfide-bond 114 .127
 FT Disulfide-bond 135 .162
 FT Cleavage-site 143 .144
 FT /note= "proteolytic site"
 FT Modified-site 145
 FT /note= "glycosylation site"
 FT Disulfide-bond 159 .164
 FT Disulfide-bond 178 .194
 FT Active-site 193
 FT Active-site 242
 FT Cleavage-site 290 .291
 FT /note= "proteolytic site in unmodified factor VII"
 FT Misc-difference 290
 FT /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT Disulfide-bond 310 .329
 FT Cleavage-site 315 .316
 FT /note= "proteolytic site"
 FT Modified-site 322
 FT /note= "glycosylation site"
 FT Disulfide-bond 340 .368
 FT Cleavage-site 341 .342
 FT /note= "proteolytic site"
 FT Active-site 344
 FT Cleavage-site 392 .393
 FT /note= "proteolytic site"
 FT Cleavage-site 396 .397
 FT /note= "proteolytic site"
 FT Cleavage-site 402 .403
 FT /note= "proteolytic site"
 US5580560-A.
 XX 03 -DEC-1996.
 XX 22-AUG-1994; 94US-00293778.
 XX 13 -NOV-1989; 89US-00434149
 PR 12 -JUN-1992; 92US-0098248
 PR 09 -AUG-1993; 93US-00104509.
 PA (NOVO) NOVO-NORDISK AS.
 XX Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
 PA WPI; 1997-033523/03.
 XX Mutated human factor VII or VIIa proteins - with amino acid substitutions
 PT to improve proteolytic stability.
 XX Example 3 ; Page: 28pp; English.
 CC Modified human factor VII or VIIa proteins are stabilised against
 CC one of the residues Lys32, Lys38,
 CC Lys42, Tyr44, Phe28, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an
 CC amino acid that provides a proteolytically more stable peptide bond,
 CC provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
 CC The modified proteins are useful for treating bleeding disorders such as
 CC thrombocytopenia and von Willebrand's disease. They are also suitable for
 CC addition to plasma substitutes. The present sequence is a specific
 CC example of a modified factor VII protein. (Updated on 25-MAR-2003 to
 CC correct PF field.)
 XX SQ Sequence 406 AA;
 Query Match Score 172; DB 2; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1.2e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 ANAFLXXLRPGSLRXCXXOCFSXXARXIFKDAXRKLFWISY 44
 Db 1 ANAFILELRPGSLERECKEQQSFEAREIFKDAERRKLFWISY 44
 RESULT 10
 AAU77745 ID AAU77745 standard; protein; 406 AA.
 XX
 AAU77745; AC
 XX DT 05-JUN-2002 (first entry)
 DE Human-factor VII active site mutant.
 XX Factor VII; human; shock heat treatment; protein stability;
 KW protein manufacture; protein conformation; mutant; mutant.
 XX OS Homo sapiens.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 Key 193
 /note= "Member of the factor VII catalytic triad"
 FT Active-site 242
 /note= "Member of the factor VII catalytic triad"
 FT FT
 FT Misc-difference 344
 /label= Gly, Met, Thr
 /note= "Preferably Ala. Wild type Ser"
 FT Active-site 344
 /note= "Member of the factor VII catalytic triad"
 FT FT
 XX WO20017141-A1.
 PN XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-DK000234.
 PP XX
 PR 06-APR-2000; 2000DK-00000073.
 PR 17-APR-2000; 2000US-0197650P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Matthiesen F;
 DR WPI; 2001-657162/75.
 XX Stabilization of a polypeptide e.g. in a pharmaceutical composition
 PT involves a shock heat treatment.
 XX Disclosure; Page: 22pp; English.
 PS
 CC The invention describes a method of stabilising a polypeptide involving
 CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition, in the industrial or large scale method of
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified human
 CC factor VII protein, mutated at the catalytic site, described in the
 CC invention. Note: This sequence does not appear in the specification but
 CC has been obtained using information given in the invention
 CC

FT	Arg-Lys-Thr-Leu"	
XX	JP20001061479-A.	
PN		
XX		
PD	13-MAR-2001.	
XX		
PF	24-AUG-1999; 99JP-00237610.	
XX		
PR	24-AUG-1999; 99JP-00237610.	
XX		
(KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.		
XX		
WPI:	2001-310677/33.	
DR	N-PSDB; AAH19462.	
XX		
PT	Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of hemophilia.	
XX		
PS	Claim 9; Page 17-18; 29pp; Japanese.	
XX		
CC	The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-30. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients	
XX		
SQ	Sequence 406 AA;	
Query Match	Score 172; DB 4; Length 406;	
Best Local Similarity	77.3%; Pred. No. 1.2e-20;	
Matches	34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
XX		
Qy	1 ANAFLXXLRPGSLXRXCKXXQCSPXXARXIFKDAKRTKLFWISY 44	
Db	1 ANAFLLELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 44	
XX		
RESULT 15		
ID	AAM52183 standard; protein; 406 AA.	
XX		
AC	AAM52183;	
XX		
DT	07-FEB-2002 (first entry)	
XX		
DE	Human FVII mutant V253N.	
XX		
KW	Factor VII; FVII; Factor VIII; FVIII; haemostatic; thrombolytic; cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease; myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant; muttein.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	
FT	Misc-difference 6	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 7	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 14	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 16	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 19	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 20	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 25	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Misc-difference 26	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	Modified-site 52	
FT	/note= "O-glycosylated"	
FT	Modified-site 60	
FT	/note= "O-glycosylated"	
FT	Modified-site 145	
FT	/note= "N-glycosylated"	
FT	Cleavage-site 152 - 153	
FT	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a	

PT Misc-difference 253 single disulphide bridge"
 PT /note= "Wild-type Val substituted by Asn"
 PT Modified-site 322
 PT /note= "N-glycosylated"
 XX
 PN WO200158935-A2.
 XX PD 16-AUG-2001.
 XX 12-PFB-2001; 2001WO-DK0000094.
 XX PR 11-PFB-2000; 2000DK-00000218.
 XX PR 18-OCT-2000; 2000DK-00001558.
 XX PA (MAXY-) MAXYGEN APS.
 XX PI Andersen KV, Pedersen AH, Bornae C;
 XX DR 2001-581807/65.
 XX PT New conjugate, useful for treating Factor VIIA related diseases or
 PT disorders such as hemophilia, liver disease, myocardial infarction and
 PT deep vein thrombosis, comprises non-polypeptide group covalently attached
 PT to polypeptide group.
 XX PS Example 3; Page: 89pp; English.
 XX The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIA)
 CC polypeptide conjugates, comprising at least one non-polypeptide group,
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC the polypeptide differs from that of the wildtype FVIIA (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the non-
 CC polypeptide group has been introduced or removed. The FVIIa conjugates
 CC have haemostatic, thrombolytic, cardiac, hepatotoxic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity. Note: The present sequence is not shown in the
 CC specification but is derived from the human wild-type FVII sequence shown
 CC in SEQ ID NO 1 (AAM52171)
 XX SQ Sequence 406 AA;
 Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ANAFLXXLRPESLXRCKXQCSPEXXARXFKDARTKLFWIISY 44
 Db 1 ANAFLXXLRPESLXRCKXQCSPEXXARXFKDARTKLFWIISY 44

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	466	1 KFHU7	coagulation Factor VIIa
2	138	71.9	443	2 KFHU7	coagulation Factor VIIa
3	123	64.1	407	1 KFB07	coagulation Factor VIIa
4	109	56.8	461	1 JX0210	protein C (activator)
5	104	54.2	456	1 KXBO	protein C (activator)
6	102	53.1	488	1 EXHU	coagulation Factor VIIa
7	101	52.6	492	1 EXBO	coagulation Factor VIIa
8	100	52.1	461	1 S18994	protein C (activator)
9	96	50.0	482	1 EXRT	coagulation Factor VIIa
10	91	47.4	475	1 EXCH	coagulation Factor VIIa
11	86	44.8	416	1 KFBO	protein C (activator)
12	84	43.8	461	1 KXHU	coagulation Factor VIIa
13	83	43.2	461	1 KFHU	coagulation Factor VIIa
14	83	43.2	622	1 TBHU	thrombin (EC 3.4.2)
15	79	41.1	617	2 S10511	thrombin (EC 3.4.2)
16	79	41.1	618	2 A35827	thrombin (EC 3.4.2)
17	78	40.6	452	1 A30351	coagulation Factor X
18	78	40.6	459	2 J00419	probable MAP kinases
19	71.5	37.2	576	2 S96763	plasma protein S
20	69	35.9	642	2 S53433	plasma protein S
21	66	34.4	675	1 KXBO5	plasma protein S
22	65.5	34.1	594	2 D84859	probable MAP kinases
23	65.5	34.1	603	2 S53434	plasma protein S
24	64	33.3	642	2 S53434	plasma protein S
25	64	33.3	646	2 S38819	plasma protein S
26	64	33.3	676	1 KXHUS	plasma protein S
27	63	32.8	396	1 KXBOZ	plasma protein S
28	63	32.8	625	1 TBBO	thrombin (EC 3.4.2)
29	63	32.8	675	1 KXRRT	plasma protein S

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM Protein - Protein search, using SW model

Run on: August 22, 2005, 09:19:07 ; Search time 15 Seconds
(without alignments)
282.236 Million cell updates/sec

Title: US-10-031-005-3
Perfect score: 192
Sequence: 1 ANAFLXXLRPGSLXRCKXX.....XXARLIFKDXRTKLFWIISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

RESULT 1
KFHU7
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1983 #sequence revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: A28322; A23819; A31186; B31186; S63524
R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Inslley, M.Y.; Hagen, F.S.; Murr, Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent
A;Reference number: A23819; PMID:87260948; PMID:3037537
A;Accession: A28322;
A;Molecule type: DNA
A;Residues: 1-466 <OHA>
A;Cross-references: GB:MI3232; NID:9182799; PID:AA804040.1; PID:9180334
R;Hagen, F.S.; Gray, C.L.; O'Hara, P.J.; Grant, F.J.; Woodbury, R.G.; Hart, C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A;Title: Characterization of a cDNA Coding for human Factor VII.
A;Reference number: A23819; PMID:86205965; PMID:348620
A;Accession: A23819
A;Molecule type: mRNA
A;Residues: 1-466 <HAG>
A;Cross-references: GB:MI3232; NID:9182799; PID:9182801
R;Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.; Biochemistry 27, 7785-7793, 1988
A;Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A;Accession: A31186
A;Reference number: A90539; PMID:89088153; PMID:3264725
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at
A;Accession: A40529; PMID:91204041; PMID:1904059
A;Residues: 61-212 <TH1>
A;Accession: B31186
A;Molecule type: protein
A;Residues: 213-466 <PH2>
A;Cross-references: R;Bjoern, S.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen, A.; Pedersen, E.; Petersen, L.C.; R;Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Petersen, L.C.; Biochem. 266, 11051-11057, 1991
J. Biol. Chem. 266, 11051-11057, 1991
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at
A;Accession: A40529; PMID:91204041; PMID:1904059
A;Content: annotation carbohydrate binding sites
R;Persson, E.; Petersen, L.C.; R;Persson, E.; Petersen, L.C.; Eur. J. Biochem. 234, 293-300, 1995
A;Title: Structurally distinct Ca(2+) binding sites in the gamma-carboxy
A;Reference number: S63524; PMID:8523655
A;Accession: S63524
A;Molecule type: protein
A;Residues: 61-65,99-103;105-109;213-217;308-312 <PER>
C;Genetic
A;Gene: GDB:87
A;Cross-references: GDB:119897; OMIM:227500
A;Map position: 13q34-13q34
A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C;Function:
A;Description: catalyzes the proteolytic activation of coagulation factor X in the preser
oagulation factor IX in the presence of calcium and tissue factor

A; Pathway: blood coagulation extrinsic pathway
 C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence #status predicted <SIG>
 F; 1-120/Domain: proteopeptide #status predicted <PRO>
 F; 45-104/Domain: Gla domain homology <GLA>
 F; 61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
 F; 110-141/Domain: EGF homology <EG1>
 F; 151-187/Domain: EGF homology <EG2>
 F; 213-446/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F; 213-447/Domain: G protein homology <TRY>
 F; 66, 67, 74, 76, 79, 80, 85, 86, 89, 95/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
 F; 77-82, 110-121, 115-130, 132-141, 151-162, 158-172, 174-187, 195-322, 219-224, 238-254, 370-389, 382/Modified site: carboxylic acid (Asp) #status absent
 F; 112, 120/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 123/Modified site: erythro-beta-hydroxyaspartic acid (Asn) (covalent) #status absent
 F; 212-213/Cleavage site: Arg-Tle (coagulation factor XIIa) #status experimental
 F; 353, 362, 404/Active site: His, Asp, Ser #status predicted
 F; 360-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted
 Query Match Score 89.6%; Score 172; DB 1; Length 466;
 Best Local Similarity 77.3%; Pred. No. 3 ge-21;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 ANAFLXXLRPGSLXRXCXXXQCSXXAXTIFDAXRTKLFWIWSY 44
 Db 61 ANAFLEELRPGSLRECKEQSPEEARIFDAERTKLFWIWSY 104

RESULT 2
 I46332 coagulation factor VII - rabbit
 C; Species: Oryctolagus cuniculus (domestic rabbit)
 C; Date: 04-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C; Accession: I46332
 R; Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A; Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A; Reference number: I46332; MUID:8383365
 A; Accession: I46332
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Cross-references: GB:S56300; NID:g266294; PID:g266295
 C; SuperFamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F; 1-83/Domain: Gla domain homology <GLA>
 F; 89-120/Domain: EGF homology <EG1>
 F; 130-166/Domain: EGF homology <EG2>
 F; 192-425/Domain: trypsin homology <TRY>
 Query Match Score 71.9%; Score 138; DB 2; Length 443;
 Best Local Similarity 59.1%; Pred. No. 2.1e-15;
 Matches 26; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 ANAFLXXLRPGSLXRXCXXXQCSXXAXTIFDAXRTKLFWIWSY 44
 Db 40 ANSPLLELRPGSLRECKEQELCSEEAREVFQSTERKQFWIWSY 83

RESULT 3
 coagulation factor VIIa (EC 3.4.21.21) - bovine
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C; Accession: A31979; C20274
 R; Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S., J. Biol. Chem. 263, 1468-1487, 1988
 A; Title: Bovine factor VII. Its purification and complete amino acid sequence.
 A; Reference number: A31979; MUID:89008362; PMID:3049594
 A; Accession: A31979
 A; Molecule type: protein
 A; Residues: 1-407 <TAKS>
 A; Cross-references: UNIPROT:P22457

R; McMullen, B.A.; Fujikawa, K.; Kissiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood clotting factor X. R. Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S. J. Biochem. 104, 867-868, 1988
 A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor X. A; Reference number: A44556; MUID:8921399; PMID:3149637
 A; Contents: annotation
 A; Note: structure and location of covalently bound carbohydrate
 C; Function:
 A; Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A; Pathway: blood coagulation extrinsic Pathway
 C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; coagulation factor VIIa light chain #status experimental <MA1>
 F; 1-152/Product: coagulation factor VIIa light chain #status experimental
 F; 1-44/Domain: Gla domain homology (fragment) <GLA>
 F; 50-81/Domain: EGF homology <EG1>
 F; 91-127/Domain: EGF homology <EG2>
 F; 153-387/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F; 153-387/Domain: trypsin homology <TRY>
 F; 16, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
 F; 17-22, 50-61, 55-70, 72-81, 91-102, 98-112, 114-127, 135-262, 159-164, 178-198, 310-329, 340-368/I
 F; 52/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F; 145, 203/Binding site: carboxylic acid (Asn) (covalent) #status experimental
 F; 152-153/Cleavage site: Arg-116 (coagulation factor XIIa) #status experimental
 F; 193, 242, 344/Cleavage site: His, Asp, Ser #status predicted
 F; 290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental
 Query Match Score 64.1%; Score 123; DB 1; Length 407;
 Best Local Similarity 52.3%; Pred. No. 6.9e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 Qy 1 ANAFLXXLRPGSLXRXCXXXQCSXXAXTIFDAXRTKLFWIWSY 44
 Db 1 ANGFLBELLPGSLRECREELCSFEEHEIFRNEERTRQFWIWSY 44

RESULT 4
 JX0210 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N; Alternative names: vitamin K-dependent serine proteinase
 C; Species: Mus musculus (house mouse)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C; Accession: JX0210
 R; Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T. J. Biochem. 111, 491-495, 1992
 A; Title: Isolation and characterization of a mouse protein C CDNA.
 A; Reference number: JX0210; MUID:92316897; PMID:1618739
 A; Accession: JX0210
 A; Molecule type: mRNA
 A; Residues: 1-461 <TPD>
 A; Cross-references: UNIPROT:P31587; GB:D10445; NID:9220385; PID:9220386
 A; Experimental source: liver
 C; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that recognizes coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence #status Predicted <SIG>
 F; 1-33/Domain: Gl domain homology <GLA>
 F; 27-85/Domain: Gl domain homology <GLA>
 F; 34-41/Domain: Product: protein C #status Predicted <PRO>
 F; 42-196, 199-461/Domain: Product: protein C #status Predicted <PRC>
 F; 42-196/Domain: Light chain #status Predicted <PC>
 F; 91-130/Domain: EGF homology <EG1>
 F; 139-174/Domain: EGF homology <EG2>
 F; 199-211/Domain: heavy chain #status Predicted <PCH>
 A; Cross-references: UNIPROT:P22457

P;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
 P;212-445/Domain: trypsin homology <TRY>
 P;47,18,55,57,60,61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 P;121-139,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #statu
 P;214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 P;253,299,402/Active site: His, Asp, Ser #status predicted
 Score 56.8%; Score 109; DB 1; Length 461;
 Best Local Similarity 47.7%; Pred. No. 1.8e-10;
 Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
 Query 1 ANAFLXXLRPGSLXRXCKQCSFXKXIFKDAKRTKLFWIY 44
 Db 42 ANSFLEENRPGSLERECMEICDFFEEAQIFQIVNEDTLAFWIKY 85

RESULT 5
 KKBO
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
 N;Alternate names: autoprotrombin IIa; plasma protein C
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004
 C;Accession: A26250; A18386; A00528
 R;Long, G.L.; Balagale, R.M.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5653-5656, 1984
 A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
 A;Reference number: A26250; MUID:85014826; PMID:6091100
 A;Accession: A26250
 A;Molecule type: mRNA
 A;Residues: 1-416 <LON>
 A;Cross-references: UNIPROT: P00745
 R;Fernlund, P.; Stenflo, J.
 J. Biol. Chem. 257, 12170-12179, 1982
 A;Title: Amino acid sequence of the light chain of bovine protein C.
 A;Reference number: A18385; MUID:83007325; PMID:6896876
 A;Accession: A18385
 A;Molecule type: protein
 A;Residues: 40-194 <PER>
 A;Note: B2-Lys was also found
 R;Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
 A;Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C.
 A;Reference number: A19316; MUID:83169765; PMID:6572939
 A;Contents: annotation; revision to residue 110
 R;Stenflo, J.; Fernlund, P.
 J. Biol. Chem. 257, 12180-12190, 1982
 A;Title: Amino acid sequence of the heavy chain of bovine protein C.
 A;Reference number: A18386; MUID:83007326; PMID:6896877
 A;Accession: A18386
 A;Molecule type: protein
 A;Residues: 197-454, PV, <STE>
 R;Emson, N.L.; DeBault, L.E.; Emson, C.T.
 J. Biol. Chem. 258, 5548-5553, 1983
 A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless
 A;Reference number: A37541; MUID:83213513; PMID:6104092
 A;Contents: annotation; activation; calcium binding
 R;Johnson, A.E.; Emson, N.L.; Lau, T.M.; Emson, C.T.
 J. Biol. Chem. 258, 5554-5560, 1983
 A;Title: Structural changes required for activation of protein C are induced by Ca2+ bin
 A;Contents: annotation; activation; calcium binding
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
 s.
 C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a tetradecapeptide from the amino end of the heavy chain; this reaction is catalyzed by the thrombin-thrombomodulin complex.
 C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
 K-dependent coagulation factor X; EGF homology; Glu domain homology; trypsin homology
 C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>
 F;24-83/Domain: Glu domain homology <GLA>

F;30-39/Domain: propeptide #status predicted <PRO>
 F;40-194/Product: protein C light chain #status experimental. <LCH>
 F;98-128/Domain: EGF homology <EG1>
 F;137-172/Domain: EGF homology <EG2>
 F;197-210/Domain: protein C heavy chain #status experimental <APT>
 F;211-440/Domain: activation peptide #status experimental <TRY>
 F;45,46,53,55,58,59,60,64,65,68/Modified site: gamma-carboxyglutamic acid (Glu) #statu
 F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F;119-128,137-148,144-157,159-172,180-188,237-253,368-382,393-421/Disulfide bonds: #statu
 F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;252,298,397/Active site: His, Asp, Ser #status predicted
 F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 54.2%; Score 104; DB 1; Length 456;
 Best Local Similarity 45.5%; Pred. No. 1.3e-09;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

RESULT 6
 EXHU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N;Alternate names: Stuart factor
 C;Species: Homo sapiens (man)
 C;Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
 C;Accession: A24478; JQ0917; A42485; A220408; A21284; A20362; S39415; 154051; A00:
 R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is <
 A;Reference number: A24478; PMID:87026600; PMID:3768336
 A;Accession: A24478
 A;Molecule type: DNA
 A;Residues: 1-488 <LEY>
 A;Cross-references: UNIPROT: P00742; GB:L129413; GB:M14327; NID:9459809; PMID:AAA52764_1; I
 R;Messier, T.L.; Pitclan, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
 A;Reference number: JQ0917; PMID:91216473; PMID:1902434
 A;Accession: JQ0917
 A;Molecule type: mRNA
 A;Residues: 1-488 <MES>
 A;Cross-references: GB:MS728; NID:g182389; PID:AAA52421_1; PMID:g182390
 R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
 A;Reference number: A25853; MUID:86221713; PMID:86221713; PMID:3011603
 A;Accession: A24485
 A;Molecule type: DNA
 A;Residues: 1-15 <MIA>
 A;Experimental source: liver
 A;Note: Sequence extracted from NCBI backbone (NCBIN:93780, NCBI:P:93787)
 R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1986
 A;Title: Isolation and characterization of human blood-coagulation factor X cDNA
 A;Accession: A25853
 A;Molecule type: mRNA
 A;Residues: 19-284, 'E' 289-488 <KAU>
 R;Fung, M.R.; Hay, C.W.; Macmillay, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A;Title: Characterization of an almost full-length cDNA coding for human blood coagulat
 A;Accession: A22208
 A;Molecule type: mRNA
 A;Residues: 13-441, 'S' 443-488 <FON>
 A;Cross-references: GB:M22613; NID:g180335; PID:AAA51984_1; PMID:g180336
 R;Leytus, S.P.; Chung, D.W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A;Title: Characterization of a cDNA coding for human factor X.
A;Reference: A21284; MUID:84222026; PMID:6587384
A;Molecule type: mRNA
A;Residues: 13-284; 'E', 289-488 <LE2>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation fact
A;Reference number: A20362; MUID:83257207; PMID:6871167
A;Molecule type: protein
A;Residues: 41-179 <MCN>
R;Iruo, K.; Morita, T.
Bur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A;Reference: S39414; MUID:94062825; PMID:8243461
A;Molecule type: protein
A;Residues: 183-234 <ING>
A;Note: Glycosylation sites
A;Note: Identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hansabhuhanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A;Reference: 154051; MUID:90128299; PMID:2612918
A;Accession: 154051
A;Status: translation not shown; translated from GB/EMBL/DBDB
A;Molecules: 1-23 <RES>
A;Cross-references: GB:M33297; NID:gi183860; PID:AAA52636_1; PID:9553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human ds(1-45) factor Xa at 2.2 angstroms resolution.
A;Contents: annotation: A4958; PMID:83558; MUID:9336077; PMID:104579
A;Map position: 1q34-13q34
A;Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
C;Comment: The two chains held together by one disulfide bond are formed from a single-c
C;Comment: The activation peptide is cleaved by factor Ixa (in the intrinsic pathway) or
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: GDB:119890; OMIM:227600
C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam F;183-234/Domain: signal sequence #status predicted <SIG>
F;24-40/Domain: propeptide #status predicted <PRO>
F;23-84/Domain: Glu domain homology <LCH>
F;41-179/Domain: coagulation factor X light chain #status experimental <LCH>
F;90-121/Domain: EGF homology <EG1>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-234/Domain: activation Peptide #status experimental <APt>
F;235-488/Product: coagulation Factor Xa heavy chain #status experimental <ACT>
F;44-47,54,65,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat F;57-62/Disulfide bonds: #status experimental <TRY>
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/ F;199-211/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;221-221/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;34-245/Cleavage site: Arg-Lle (coagulation factor IXa, coagulation factor VIIa) #stat F;276,322,419/Active site: His, Asp, Ser #status experimental
Query Match 53.1%; Score 102; DB 1; Length 488;
Best Local Similarity 40.9%; Pred. No. 2.e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
Qy 1 ANAFLXXLRPGSLXRXCXQCSFXXXARXFKDAXRTKLFWISY 44

A;Contents: sulfate binding
 C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C;Comment: The two chains are formed from a single-chain precursor by the excision of two activation peptide.

C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong affinity, to the gamma-carboxyglutamic acid (Gla) residues and, with strong affinity, to the gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin K-dependent modification of the polypeptide chain.

C;Genetics:
 A;Gene: F10
 A;Map position: 13q34
 C;Function:
 A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the prothrombinase complex.
 A;Pathway: blood coagulation

C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology

C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate

F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-40/Domain: propeptide #status predicted <PRO>
 F;25-84/Domain: Glu domain homology <GLA>
 F;41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F;90-121/Domain: EGF homology <EG1>
 F;129-164/Domain: EGF homology <EG2>

F;183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F;183-233/Domain: activation peptide #status experimental <APT>
 F;234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F;45-461/Domain: trypsin homology <TRY>

F;45-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status F
 F;57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-181/Disulfide bonds: #status F
 F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F;200/Binding site: sulfatase <tyr> (covalent) (partial) #status experimental
 F;208/485/Binding site: carbohydrate (thr) (covalent) #status experimental
 F;233-234/Cleavage site: Arg-116 (coagulation factor VIIa) #status experimental
 F;240-245, 260-276, 389-403, 414-442/Disulfide bonds: #status experimental

F;275,321-418/Active site: His, Asp, Ser #status predicted

Query Match Score 101; DB 1; Length 492;
 Best Local Similarity 43.2%; Pred. No. 4.3e-09;
 Matches 19; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPSSLXKRACKXQCSFXKARXIFKDARTKLWISY 44
 Db 41 ANSFLEEVKGQNLERECLTEACSLBEEREVFEADAEQTDFWSKY 84

RESULT 8

S1894
 protein C (activated) (EC 3.4.21.69) precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: S18994; S24312
 R;Otafugi, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 A;Description: The cDNA cloning and mRNA expression of rat protein C.
 A;Reference number: S18994
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Accessories: 1-161 <OKA>
 A;Cross-references: UNIPROT:P31394; EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963
 R;Otafugi, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992
 A;Title: The cDNA cloning and mRNA expression of rat protein C.
 A;Reference number: S24312; MUID:93329550; PMID:627650
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Accessories: 1-161 <OKA>
 A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963
 C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolyase; serine proteinase
 F;1-12/Domain: signal sequence #status predicted <SIG>
 F;27-85/Domain: Glu domain homology <GLA>
 F;41-179/Domain: coagulation factor X light chain #status predicted <LCH>
 F;33-42/Domain: propeptide #status predicted <PRO>

F;43-461/Product: protein C #status predicted <PRC>
 F;91-130/Domain: EGF homology <EG1>
 F;113-174/Domain: EGF homology <EG2>
 F;211-445/Domain: trypsin homology <TRY>
 F;47,48,55,57,60,61,66,67,70,7/Modified site: gamma-carboxyglutamic acid (Glu) #status I
 F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F;121-130,139-150,146-159,161-174,182-320,239-255,373-387,398-426/Disulfide bonds: #status I
 F;215,291/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;254,300,402/Active site: His, Asp, Ser #status predicted

Query Match Score 100; DB 1; Length 461;
 Best Local Similarity 45.5%; Pred. No. 6.1e-09;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPSSLXKRACKXQCSFXKARXIFKDARTKLWISY 44
 Db 42 ANSFLEEVKGQNLERECLTEACSLBEEREVFEADAEQTDFWSKY 85

RESULT 9

coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
 C;Accession: S49075; JCA670; PS0190; PS0191; PS0190; PS0191; PS0190; PS0191
 R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A;Title: Evidence for competition between vitamin K-dependent clotting factors for intracelluar substrates
 A;Reference number: A58498; MUID:9609336; PMID:8578539
 A;Accession: S49075
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:063207; EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:950666
 A;Note: submitted to the EMBL Data Library, June 1994
 A;Note: neither the complete nucleic acid sequence nor the complete translation are shown
 R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A;Reference number: JC4670; MUID:96194815; PMID:86474760
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA1>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA2>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA3>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA4>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA5>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <STA6>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ1>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ2>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ3>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ4>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ5>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ6>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ7>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ8>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ9>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ10>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ11>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ12>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ13>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ14>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ15>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ16>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ17>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ18>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ19>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ20>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ21>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ22>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ23>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ24>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ25>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ26>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ27>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ28>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ29>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ30>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ31>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ32>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ33>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ34>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ35>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ36>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ37>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ38>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ39>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ40>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ41>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ42>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ43>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ44>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ45>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ46>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ47>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ48>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ49>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ50>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ51>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ52>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ53>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ54>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ55>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ56>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ57>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ58>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ59>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ60>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ61>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ62>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ63>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ64>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ65>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ66>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ67>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ68>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ69>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ70>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ71>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ72>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ73>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ74>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ75>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ76>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ77>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ78>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ79>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ80>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ81>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ82>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ83>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ84>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ85>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ86>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ87>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ88>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ89>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ90>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ91>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ92>
 A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A;Molecule type: protein
 A;Accessories: 1-482 <ENJ93>
 A;Cross-references: EMBL:X79

Qy F1129-164/Domain: EGF homology <EG2>
 F1132-231/Product: coagulation factor X heavy chain #status predicted <HCH>
 F122-482/Domain: activation peptide #status predicted <APT>
 F122-482/Domain: coagulation factor Xa heavy chain #status predicted <ACT>
 F145-47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F15-57, 62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 41
 F1137/Binding site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F1208/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F1208/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F211-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status
 F214, 320, 417/Active site: His, Asp, Ser #status predicted

Query Match Score 96; DB 1; Length 482;
 Best Local Similarity 40.9%; Pred. No. 3e-08;
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRLRGSLLXRXCXQCSFXXARXKIFDAXRTKLFWIISY 44
 Db 41 ANSFFEEIKGNLBEFCEBICSPBEEFEDNEKTEFWNKY 84

RESULT 10
 EXCH coagulation factor Xa (EC 3.4.21.6) precursor - chicken
 N:Alternate names: virus-activating proteinase
 C:Species: Gallus gallus (chicken)
 C:Date: 12-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S15838; S20380; S20381
 R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na
 FEBs Lett. 28:, 281-285, 1991
 A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
 A:Reference number: S15538; MUID:91257322; PMID:2044767
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Cross-references: UNIPROT:P25155; DDBJ:D00844; PIDN:BAA00724_1; PID:g2228
 R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
 FEBs Lett. 298, 274-278, 1992
 A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
 A:Reference number: S20380; MUID:92164779; PMID:1537403
 A: Molecule type: protein
 A:Residues: 1-475 <SUZ>
 A:Accession: S20381
 A:Molecule type: protein
 A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
 C:Function: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F1120/Domain: signal sequence #status predicted <SIG>
 A:Pathway: blood coagulation
 A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F122-40/Domain: propeptide #status predicted <PRO>
 F12-84/Domain: Gla domain homology <GHA>
 F41-185/Domain: coagulation factor X light chain #status experimental <LCH>
 F9-121/Domain: EGF homology <EG1>
 F12-167/Domain: EGF homology <EG2>
 F186-475/Modified site: coagulation factor X heavy chain #status predicted <HCH>
 F186-475/Domain: activation peptide #status predicted <APT>
 F241-475/Domain: coagulation factor Xa heavy chain #status experimental <APC>
 F241-468/Domain: trypsin homology <TRY>
 F16-47, 54, 56, 59, 60, 65, 66, 69, 72, 79/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F15-62, 90-101, 95-110, 112-121, 129, 140, 136-152, 154-167, 175-348, 247-252, 267-283, 396-410, 42
 F196-207, 228/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F196-207, 228/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F212, 328, 425/Active site: His, Asp, Ser #status predicted

Query Match Score 91; DB 1; Length 475;
 Best Local Similarity 38.6%; Pred. No. 2.1e-07;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRLRGSLLXRXCXQCSFXXARXKIFDAXRTKLFWIISY 44
 Db 41 ANSFFEEIKGNLBEFCEBICSPBEEFEDNEKTEFWNKY 84

RESULT 11
 KFBO coagulation factor IXa (EC 3.4.21.22) precursor - bovine
 N:Alternate names: Christmas factor
 C:Species: Bos primigenius taurinus (cattle)
 C:Date: 30-Nov-1980 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
 C:Accession: A14157; B20274; I15891; A00923
 R:Katayama, K.; Erickson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, B.W.; Tit
 Proc. Natl. Acad. Sci. U.S.A. 76, 4390-4394, 1979
 A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fac
 A:Reference number: A14757; MUID:80056619; PMID:291916
 A:Accession: A14757
 A:Molecule type: protein
 A:Residues: 1-63, 'T', 65-416 <CAT>
 A:Cross-references: UNIPROT:P04741
 R:McMullen, B.A.; Fujikawa, K.; Kisieli, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526
 A:Accession: B20274
 A:Molecule type: protein
 A:Residues: 59-63, 'X', 65-69 <CHO>
 A:Cross-references: GB:J00007; PIDN:91613053; PIDN:AAA30520_1; PID:91613054
 R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
 Nature 299, 178-180, 1982
 A:Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
 A:Reference number: I145891; MUID:82272386; PMID:6237289
 A:Accession: I145891
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 52-139 <CHO>
 A:Cross-references: GB:J00007; PIDN:91613053; PIDN:AAA30520_1; PID:91613054
 A:Title: A new triosaccharide sugar chain linked to a serine residue in bovine blood coag
 A:Reference number: A44556; MUID:89213999; PMID:3149637
 A:Contents: annotation
 A:Note: structure and location of a carbohydrate covalently bound to Ser
 C:Comment: Factor IX is activated by factor Xa, which excises the activation peptide pro
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homolog
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F1-146/Product: coagulation factor IXa light chain #status experimental <GLA>
 F1-146/Domain: Gla domain homology (fragment) <GL1>
 F51-82/Domain: EGF homology <EG1>
 F88-124/Domain: EGF homology <EG2>
 F147-181/Domain: activation peptide #status experimental <APT>
 F182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F182-409/Domain: trypsin homology <TRY>
 F7, 8, 15, 1, 20, 21, 26, 127, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #stat
 F18-23, 51-62, 56-71, 73-82, 88-99, 109, 111-124, 132-290, 207-223, 331-351, 362-390/Disulfide
 F153/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F164/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F158, 168, 173, 261/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F1, 222, 270, 366/Active site: His, Asp, Ser #status predicted

Query Match Score 86; DB 1; Length 416;
 Best Local Similarity 44.1%; Pred. No. 1.3e-06;
 Matches 15; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 11 GSIXRXCXQCSFXXARXKIFDAXRTKLFWIISY 44
 Db 12 GNLERECKEKCSEEEAREVFENTKETFWKQY 45

RESULT 12
KXHU
 Protein C (activated) (EC 3.4.21.69) precursor - human
 N;Alternate names: autoprothrombin IIa; plasma protein C
 C;Species: Homo sapiens (man)
 C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004
 C;Accession: A22331; A25426; A21781; A23789; A00927;
 R;Foster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A;Title: The nucleotide sequence of the gene for human protein C.
 A;Reference number: A22331; MUID:85270390; PMID:2991887
 A;Molecule type: DNA
 A;Residues: 1-461 <POS1>
 A;Cross-references: UNIPROT:P04070; GB:M11228; PIDN:9190333; PIDN:AAA60166_1; PMID:g190334
 R;Plutzky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-551, 1986
 A;Reference number: A25426; MUID:86120978; PMID:3511471
 A;Accession: A25426
 A;Molecule type: DNA
 A;Residues: 'Q',1-45-'L',446-461 <PLU>
 A;Cross-references: GB:K0259; PIDN:9190322; PIDN:AAA60164_1; PIDN:g190323
 R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzyk, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5333-5327, 1985
 A;Title: Characterization of a cDNA coding for human protein C.
 A;Reference number: A21781; MUID:84272714; PMID:6589623
 A;Accession: A21781
 A;Molecule type: mRNA
 A;Residues: 'Q',1-45-'L',446-461 <POS2>
 A;Cross-references: GB:K02059; PIDN:9190322; PIDN:AAA60164_1; PIDN:g190323
 R;Beckmann, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzyk, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5333-5327, 1985
 A;Title: The structure and evolution of a 461 amino acid human protein C precursor and its
 A;Reference number: A23789; MUID:85269639; PMID:2991859
 A;Accession: A23789
 A;Molecule type: mRNA
 A;Residues: 1-161 <BEC>
 A;Cross-references: GB:X02750; PIDN:935689; PIDN:CAA26528_1; PIDN:g9763120
 R;Miletich, J.P.; Broze Jr., G.J.; Spellman, M.W.
 J. Biol. Chem. 267, 11397-11404, 1992
 A;Title: Beta protein C is present in the first epidermal growth factor domain of factor Va.
 A;Reference number: A44606; MUID:9029304; PMID:1694179
 A;Contents: annotation; carbohydrate binding sites; activation peptide
 A;Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A;Title: O-linked fucose is present in the first epidermal growth factor domain of factor Va.
 A;Reference number: A44606; MUID:9218470; PMID:1544894
 A;Contents: annotation; beta-hydroxyaspartic acid
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that is activated by complexing with protein S. Protein C also activates factor Va by enhancing the activation of factor Va by complexing with protein S. Protein C is synthesized in the liver as a single chain precursor, which is cleaved into two chains by a dodecapeptide from the amino end of the heavy chain; this reaction, C;Genetics: A;Gene: GDB:PROC
 A;Cross-references: GDB:120317; OMIM:176860
 A;Map position: 2q13-2q21
 A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
 C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 P;1-32/Domain: signal sequence #status predicted <SIG>
 P;1-32/Domain: Glu domain homology <GLA>
 P;2-86/Domain: Propeptide #status predicted <PRO>
 A;Intrns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
 C;Comment: protein C light chain #status predicted <LCH>
 P;93-197/Product: protein C heavy chain #status predicted <HCH>
 P;140-175/Domain: EGF homology <EG1>
 P;200-461/Product: protein C heavy chain #status predicted <HCH>
 A;Cross-references: GB:J00137; PIDN:g182610; PMID:9182611
 F;2-12/445/Domain: trypsin homology <TRY>
 F;48-49, 56-58, 61, 62, 67, 71/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
 F;59-64, 92-105, 101-120, 122-131, 140-151, 147-160, 162-175, 183-319, 238-254, 373-387, 398-426/1
 A;Cross-references: GB:J00137; PIDN:g182610; PMID:9182611

P;106-111/Disulfide bonds: #status predicted
 P;110/Binding site: carbohydrate (thr) (covalent) #status absent
 P;113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 P;139-290,355/Binding site: carboxyhydrate (Asn) (covalent) #status experimental
 P;211-212/Cleavage site: Arg-Lysine (thrombin) #status experimental
 P;251-299,402/Active site: His, Asp, Ser #status predicted
 P;371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical
 Query Match 43.8%; Score 84; DB 1; Length 461;
 Best Local Similarity 43.9%; Pred. No. 3.1e-06;
 Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 ANAFIXLXRPGSLKXCKXXQCSFXARXKFIDAXRTKLEW 41
 Db 43 ANSFLEBLRSSLERBCIEICDFEEAKETFQNVDLTLAFW 83
 RESULT 13
KPHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N;Alternate names: antihemophilic factor B; Christmas factor
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A00922; A37570; A30511; A32673; A21337; A37546; A60486; A20;
 R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A;Reference number: A00922; MUID:86000558; PMID:2994716
 A;Accession: A00922
 A;Molecule type: DNA
 A;Residues: 1-461 <ANS>
 A;Cross-references: UNIPROT:P00740; GB:K02402; NID:g182612; PIDN:9182610; PIDN:9182613
 R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, P.; Gould, K.; Huddleston, J.A.; Brov
 BMJ J. 3, 103-106, 1984
 A;Title: The gene structure of human anti-haemophilic factor IX.
 A;Reference number: A37570; MUID:84236100; PMID:6329734
 A;Accession: A37570
 A;Molecule type: DNA
 A;Residues: 1-461 <ANS>
 A;Cross-references: GB:K02048
 R;Raitsma, P.H.; Bertina, R.M.; Bloos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A;Reference number: A30511; MUID:88327116; PMID:3416069
 A;Accession: A30511
 A;Molecule type: DNA
 A;Residues: 1-461 <REI>
 A;Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245_2; PID:94469253
 R;Koobert, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A;Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A;Reference number: A32989
 A;Accession: A32989
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 10-92 <KOB>
 R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; St
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A;Title: Evidence for a prevalent diomerism in the activation peptide of human coagulat
 A;Reference number: A22673; MUID:85190593; PMID:3857619
 A;Molecule type: mRNA
 A;Residues: 1-193, 'T', 195-461 <MC>
 A;Cross-references: GB:MI1309; PIDN:g180552; PIDN:AAA52023_1; PID:9180553
 A;Note: the authors translated the codon ACA for residue 29 as Tyr
 R;Jaye, M.; de la Salle, H.; Schamber, F.; Balland, A.; Kohli, V.; Findeli, A.; Tolstoshe
 Nucleic Acids Res. 11, 2325-2335, 1983
 A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
 A;Reference number: A21337; MUID:8322078; PMID:6687940
 A;Cross-references: A21337
 A;Molecule type: mRNA
 A;Residues: 1-193, 'T', 195-461 <MC>
 A;Cross-references: GB:J00137; PIDN:g182610; PMID:9182611

- R.; Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Sonat. Cell Mol. Genet. 10, 465-473, 1984
 A;Title: Isolation and characterization of human factor IX cDNA: identification of Taq I
 A;Reference number: A37546; PMID:84300526; MUID:6089357
 A;Molecule type: RNA
 A;Residues: 38-193, 'T', 195-326 <JAG>
 A;Cross-references: GB:M35672
 R;Kurachi, K.; Davie, E.W.
 A;Cross-references: GB:J00136; NID:gi182606; PIDN:AAA98726.1; PID:9182609
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A;Experimental source: liver
 R;Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A;Title: Development of an immunoaffinity process for factor IX purification.
 A;Reference number: A60486; MUID:90194857; PMID:2316207
 A;Accession: A60486
 A;Molecule type: protein
 A;Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biophys. Res. Commun. 115, 8-14, 1983
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX
 A;Reference number: A22274; PMID:8330813; PMID:6688526
 A;Accession: A20274
 A;Molecule type: protein
 A;Residues: 105-109, 'X', 111-115 <MCM>
 R;Balland, A.; Faure, T.; Carvalho, D.; Cordier, P.; Ulrich, B.; Fournet, B.; de la Sallie, P.; Tallat, S.; Perraud, P.; Dallemands, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulien, P.; EMBO J. 9, 3295-3301, 1990
 A;Title: Characterisation of two differently processed forms of human recombinant factor IX
 A;Reference number: S02527; PMID:3280312
 A;Accession: S02527
 A;Molecule type: protein
 A;Residues: 29-63 <BAL>
 A;Note: processed forms expressed in recombinant system
 R;Barford, P.A.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell, P.; Haenost, 70, 370-371, 1993
 A;Title: The first EGF-like domain from human factor IX contains a high-affinity calcium channel binding domain
 A;Reference number: S12058; PMID:91006024; PMID:2209546
 A;Accession: S12058
 A;Molecule type: mRNA; protein
 A;Residues: 1-68 <JAL>
 A;Note: processed forms expressed in recombinant system
 R;Barford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Grunbaum, M.L.; Baas, M.J.; Wiesel, M.L.; Schwartz, A.; Sommer, S.S.
 Science 239, 491-494, 1988
 A;Title: Genomic amplification with transcript sequencing.
 A;Accession: 159529; PMID:88127096; PMID:3340835
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 444-461 <RES>
 A;Cross-references: GB:S66752; NID:gi439773; PIDN:AB28588.1; PID:9439774
 R;Stofflet, E.S.; Koebel, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A;Title: Genomic amplification with transcript sequencing.
 A;Accession: 159529; PMID:88127096; PMID:3340835
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 290-339 <RE2>
 A;Cross-references: GB:MI19063; NID:gi182622; PIDN:AAA52456.1; PID:9182623

Query Match Similarity 43.2%; Score 83; DB 1; Length 461;
 Best Local Similarity 44.1%; Pred. No. 4.6e-06; Indels 0; Gaps 0;

Matches 15; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 11 GSLXRXCKXXQCSEXXARXIFKDAARTKLWISY 44
 Db 58 GNLERCMEKCSPEEARVEFENTERTTEFWKQY 91

RESULT 14

TBHU

N;Alternate names: coagulation factor II

N;Contains: prothrombin

N;Species: Homo sapiens (man)

C;Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 09-Jul-2004

C;Accession: A29351; A00914; B00914; A37549; A37550; 151952

R;Degen, S.J.; MacGillivray, R.T.A.; Davie, E.W.

Biochemistry 26 : 6165-6177, 1987

A;Title: Nucleotide sequence of the gene for human prothrombin.

A;Reference: A29351; MUID:88077877; PMID:2825773

A;Accession: A29351

A;Molecule type: DNA

A;Residues: 1-122 <DEBG>

A;Cross-references: UNIPROT:P00734; GB: M17262; GB: M33691; NID: 9558069; PIDN: AAC63054.1;

R;Degen, S.J.; MacGillivray, R.T.A.; Davie, E.W.

Biochemistry 22 : 2057-2057, 1983

A;Title: Characterization of the complementary deoxyribonucleic acid and gene coding for

A;Reference number: A00914; MUID:83231469; PMID:6305467

A;Molecule type: mRNA

A;Residues: 8-163, 'N', 165-622 <DE2>

A;Cross-references: GB: V00595; GB: J00307; NID: 937128; PIDN: CAA23842.1; PID: g1335344

A;Accession: B00914

A;Molecule type: DNA

A;Residues: 188-311 <DEB3>

R;Walz, D.A.; Hewett-Emmett, D.; Seeger, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74 : 1969-1972, 1977

A;Accession: A37549; MUID: 77193964; PMID: 2667177

A;Molecule type: protein

A;Accession: A37549

R;Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252 : 4942-4957, 1977

A;Title: Primary structure of human prethrombin 2 and alpha-thrombin.

A;Reference number: A37550; MUID: 77207112; PMID: 773923

A;Accession: A37550

R;Rabiet, M.J.; Blashill, A.; Purie, B.; Purie, B.C.

J. Biol. Chem. 261 : 13210-13215, 1986

A;Reference number: A37551; MUID: 87008532; PMID: 3759958

A;Contents: annotation; activation cleavages

R;MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.

Ann. N. Y. Acad. Sci. 485 : 73-79, 1986

A;Title: Recombinant genetic approaches to functional mapping of thrombin.

A;Reference number: 151952; MUID: 87182874; PMID: 3471151

A;Accession: 151952

A;Status: translated from GB/EMBL/DDBJ

A;Residues: 1-2, 'R', 5-100 <RES>

A;Cross-references: GB: M33031; NID: 9190723; PIDN: AAA60220.1; PID: g190724

C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin

C;Superfamily: thrombin; Glu domain homology; kringle homology; trypsin homology

C;Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplicate

F;1-24/Domain: signal sequence #status predicted <PRO>

F;25-43/Domain: propeptide #status predicted <PRO>

F;28-87/Domain: Glu domain homology <GLA>

F;44-622/Product: prothrombin #status experimental <MAT>

F;44-327/Domain: activation peptide #status experimental <APT>

F;108-186/Domain: kringle homology <KR1>

F;213-291/Domain: kringle homology <KR2>

F;328-363/Product: thrombin light chain #status experimental <LCH>

F;364-622/Product: thrombin heavy chain #status experimental <HCH>

F;364-612/Domain: trypsin homology <TRP>

F;49,50,57,59,62,63,68,69,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status &

F;60,65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status I

F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;336-482,536-550,564-594/Disulfide bonds: #status predicted

F;391-407/Disulfide bonds: #status experimental

F;406,462/Active site: His, Asp #status predicted

F;416,462/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;568/Active site: Ser #status experimental

RESULT 15

S10511

thrombin (EC 3.4.21.5) precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 09-Jul-2004

C;Accession: S10511; A60576; B42696

R;Dhanich, M.; Monard, D.

Nucleic Acids Res. 18 : 4251, 1990

A;Title: cDNA sequence of rat prothrombin.

A;Reference number: S10511; MUID: 90332426; PMID: 2377469

A;Accession: S10511

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P18292; EMBL: X52835; NID: 956969; PIDN: CAA37017.1; PID: g56970

R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.

Endocrinology 126 : 167-175, 1990

A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.

A;Reference number: A60576; MUID: 90091942; PMID: 2293880

A;Accession: B42696

A;Molecule type: protein

A;Residues: 44-58 <HEH>

A;Authors: the authors purified the proenzyme from the estrogen-stimulated maturing rat uterus

R;Banfield, D.K.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89 : 2779-2783, 1992

A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing

A;Reference number: A42696; MUID: 92212913; PMID: 1557383

A;Accession: B42696

A;Molecule type: preliminary

A;Residues: 383-617, 'E' <BAN>

A;Cross-references: GB: M817

C;Superfamily: thrombin; Glu domain homology; kringle homology; trypsin homology

C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydroxy

F;1-24/Domain: signal sequence #status predicted <S10>

F;25-43/Domain: propeptide #status predicted <PRO>

F;28-88/Domain: Glu domain homology <GLA>

F;44-611/Product: prothrombin #status experimental <PRO>

F;109-187/Domain: kringle homology <KR1>

F;215-292/Domain: kringle homology <KR2>

F;360-603/Domain: trypsin homology <TRY>

C;Comment: The prothrombin precursor is synthesized in the liver.

C;Genetics:

A;Gene: GDB:F2

P;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
P;65-66,91-104,109-187,130-170,138-182,215-292,236-276,264-287,332-478,387-403,532-546,5
P;02,458,564/Active site: His, Asp, Ser #status predicted

Query Match	41.1%	Score 79;	DB 2;	Length 617;
Best Local Similarity	37.2%	Pred. No.	2.9e-05;	
Matches	16;	Mismatches	5;	Indels
Oy	2	NAFLXXLRPGLXRXCKQXQCSFXXARXIFKDAAXRTKLFWISY	44	0;
Db	46	SGFDEELRKGNLRECVEEQCSYEAEFALESPQDTDVFWAKY	88	Gaps 0;

Search completed: August 22, 2005, 09:33:13
Job time : 17 secs

Scoring table:	BLOSUM62	ALIGMENTS			
Gapop:	10.0 , Gapext 0.5				
Searched:	1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
Database :	UniProt-03: 1: uniprot_sprot; 2: uniprot_trembl;*				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
		SUMMARIES			
Result No.	Score	Query	Match Length	DB ID	Description
1	172	89.6	466	1 FA7_HUMAN	P08709 homo sapien
2	172	89.6	679	2 Q96P08	Q96P08 homo sapien
3	138	71.9	444	1 FA7_RABBIT	P98129 oryctolagus
4	127	66.1	446	1 FA7_MOUSE	P70375 mus musculus
5	123	64.1	407	1 FA7_BOVIN	P22457 bos taurus
6	114	59.4	459	1 PRTC_PIG	Q99122 sus scrofa
7	104	56.8	460	1 PRTC_MOUSE	P33517 mus musculus
8	104	54.2	446	1 FA7_RAT	Q8kj46 rattus norvegicus
9	104	54.2	456	1 PRTC_BOVIN	P00745 bos taurus
10	102	53.1	443	2 Q8jhc9	Q8jhc9 brachydanio
11	102	53.1	488	1 FA10_HUMAN	P00742 homo sapien
12	101	52.6	425	2 Q804x7	Q804x7 gallus gallus
13	101	52.6	492	1 FA10_BOVIN	P00743 bos taurus
14	100	52.1	461	1 PRTC_RAT	P31394 rattus norvegicus
15	100	52.1	461	2 Q68f78	Q68f78 rattus norvegicus
16	99	51.6	218	1 TMG1_HUMAN	Q8ne48 homo sapien
17	99	51.6	266	2 OBNE0K	Q8ne46 homo sapien
18	99	51.6	433	2 Q804x5	Q804x5 gallus gallus
19	98	51.0	490	1 FA10_RABBIT	Q90455 oryctolagus
20	96	50.0	482	1 FA10_RAT	Q63297 rattus norvegicus
21	95	49.5	434	2 Q7T3B6	Q7t3b6 brachydanio
22	94	49.0	340	2 Q80Y26	Q80y26 mus musculus
23	94	49.0	458	1 PRTC_RABBIT	Q28661 oryctolagus
24	94	49.0	469	2 Q9GMd9	Q9gm9 ornithorhynchus anatinus
25	94	49.0	481	1 FA10_MOUSE	Q88947 mus musculus
26	93	48.4	456	1 PRTC_CANEA	Q28278 canis familiaris
27	92	47.9	228	2 Q6IP17	Q6ip17 xenopus laevis
28	92	47.9	229	2 Q8jj40	Q8jj40 xenopus laevis
29	92	47.9	251	2 QEDDE6	Q6ded6 xenopus laevis
30	92	47.9	376	1 FA10_TROCA	P81428 tropidochis
31	92	47.9	432	2 Q6GNA2	Q6gna2 xenopus laevis

- RL J. Biol. Chem. 266:11051-11057(1991).
 RN
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanga S.;
 RT "Identification of a disaccharide (Xy1-Glc) and a trisaccharide (Xy12-Glc O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.",
 RT
 RL J. Biol. Chem. 264:20320-20325(1989).
 RN [7]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=11344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.,
 RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.",
 RT
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=6117641; PubMed=8598903; DOI=10.1038/380041a0;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Konigsberg W.H., Nemreron Y., Kirchhofer D.;
 RT "The crystal structure of the complex of blood coagulation factor VIIa with soluble tissue factor.",
 RT
 RL J. Mol. Biol. 285:2089-2104(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=91126338; PubMed=9195787; DOI=10.1006/jmbi.1998.2452;
 RA Zhang E., St Charles R., Tulinsky A.,
 RA Drakenberg T.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa inhibited by BPTI mutant.",
 RT
 RL J. Mol. Biol. 285:2089-2104(1996).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
 RA Muranyi A., Finn B.E., Gippert G.P., Forsten S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human factor VII.",
 RT
 RL Biochemistry 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meide T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected male.",
 RT
 RL Blood 78:132-140(1991).
 RN [12]
 RP VARIANT GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patracchini P., Gemmatti D., Derosa V., Pinotti M.,
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat polymorphism in the factor VII gene (F7).",
 RT
 RL Hum. Genet. 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi F.,
 RT "A missense mutation (178Cys-->Tyr) and two neutral dimorphisms (115His and 333Ser) in the human coagulation factor VII gene.",
 RT
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN [14]
 RP VARIANT.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hain I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.,
 RT "Detection of missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of factor VII gene.",
 RT
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN [15]
 RP VARIANT CHARLOTTE GLN-139 AND GLN-212.
 RX MEDLINE=94264305; PubMed=804875;
 RA Chaing S., Clarke B., Srihara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the cleavage site for activation and altering binding to tissue factor.",
 RT
 RL Blood 83:3524-3535(1994).
 RN [16]
 RP VARIANT SER-367.
 RX PubMed=7860081;
 RA Dewald G., Noethen M.M., Rutherford K.;
 RT "A common Ser/Thr polymorphism in the perforin-homologous region of human complement component C7.",
 RT
 RL Hum. Hered. 44:301-304(1994).
 RN [17]
 RP VARIANT VAL-354.
 RX MEDLINE=95072589; PubMed=7981691;
 RA Bernacari F., Casarman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically adjacent mutations causing dysfunctional coagulation factors VII (29Ala-->Val) and X (334Ser-->Pro).";
 RT
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN [18]
 RP VARIANT MIE HIS-307.
 RX MEDLINE=95064662; PubMed=7974336;
 RA Ohwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
 RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by an amino acid substitution of His (CAC) for Arg(247) (CCG) in the catalytic domain.",
 RT
 RL Thromb. Haemost. 71:773-777(1994).
 RN [19]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary deficiency causes defective secretion of the molecule.",
 RT
 RL Blood 87:5085-5094 (1996).
 RN [20]
 RP VARIANT TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=884208;
 RA Bernardi F., Casarman G., Pinotti M., Ferrareti P., di Iasio M.G.,
 RA Seligsohn U.;
 RT "Ala24Val is a common, probably ancient, mutation causing factor VII deficiency in Moroccan and Iranian Jews.",
 RT
 RL Thromb. Haemost. 76:283-291(1996).
 RN [21]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8832260;
 RA Tamary H., Promovich Y., Shalom L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korotitshevsky M., Zaizov R.,
 RA Sakuragiwa N.;
 RT "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with factor VII deficiency.",
 RT
 RL Br. J. Haematol. 101:47-49(1998).
 RN [22]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=98335711; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niizya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragiwa N.;
 RT "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with factor VII deficiency.",
 RT
 RL Br. J. Haematol. 101:47-49(1998).
 RN [23]
 RP VARIANT MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=452022;
 RA Alshihawi C., Scerri C., Gaeldies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation factor VII gene.",
 RT

DR	InterPro; IPR006209; EGF-like.	Qy	1 ANAFLIXLRLPGSLXKXXQCSFXMARLFKDAXRTKLFWISY 44
DR	InterPro; IPR0021254; Peptidase S1.	Db	42 ANSLLLEELWEGSLERECNEEQCSPEAREIFKSPETRTKQFWIVY 85
DR	InterPro; IPR001314; Peptidase S1A.		
DR	InterPro; IPR003003; Pept_Ser_Cys.		
DR	InterPro; IPR000294; VitK_dep_GLA.		
PFam	PF00008; EGF; 2.		
PFam	PF00594; Gla; 1.		
DR	PFam; PF00089; Trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPsin.		
DR	PRINTS; PR00010; EGFBLOOD.		
DR	PRINTS; PR00001; GLABLOOD.		
SMART	SM00179; EGF_CA; 1.		
DR	SMART; SM00069; GLA; 1.		
SMART	SM00020; TRYSPC; 1.		
PROSITE	PS00010; ASX_HYDROXYL; 1.		
PROSITE	PS00222; EGF_1; 1.		
PROSITE	PS01186; EGF_3; FALSE_NEG.		
PROSITE	PS00026; EGF_3; 1.		
PROSITE	PS01187; EGF_CA; 1.		
PROSITE	PS00011; GLA_1; 1.		
DR	PROSITE; PS50998; GLA_2; 1.		
DR	PROSITE; PS50240; TRYPsin_DOM; 1.		
DR	PROSITE; PS00134; TRYPsin_His; 1.		
DR	BLOOD coagulation; Calcium-binding; EGF-like domain; Hydrolases; Hydroxylation;		
KW	Gamma-carboxylglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;		
KW	Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.		
FT	SIGNAL 1 24		
FT	PROPEP 25 41		Potential.
FT	CHAIN 42 193		Factor VII light chain.
FT	CHAIN 194 446		Factor VII heavy chain.
FT	DOMAIN 42 86		Gla.
FT	DOMAIN 87 123		EGF-like 1, calcium-binding (Potential).
FT	DOMAIN 128 169		EGF-like 2.
FT	DOMAIN 129 168		Serine protease.
FT	SITE 193 194		Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin) (By similarity).
FT	ACT_SITE 234 234		By similarity.
FT	ACT_SITE 283 283		By similarity.
FT	ACT_SITE 385 385		By similarity.
FT	BINDING 379 379		Substrate (By similarity).
FT	DISUFDID 58 63		By similarity.
FT	DISUFDID 91 102		By similarity.
FT	DISUFDID 96 111		By similarity.
FT	DISUFDID 113 122		By similarity.
FT	DISUFDID 132 143		By similarity.
FT	DISUFDID 139 153		By similarity.
FT	DISUFDID 155 168		By similarity.
FT	DISUFDID 176 203		By similarity.
FT	DISUFDID 200 235		By similarity.
FT	DISUFDID 219 320		By similarity.
FT	DISUFDID 351 370		By similarity.
FT	DISUFDID 381 409		By similarity.
FT	MOD_RES 47 48		4-carboxyglutamate.
FT	MOD_RES 55 55		4-carboxyglutamate.
FT	MOD_RES 57 57		4-carboxyglutamate.
FT	MOD_RES 60 60		4-carboxyglutamate.
FT	MOD_RES 61 61		4-carboxyglutamate.
FT	MOD_RES 66 66		4-carboxyglutamate.
FT	MOD_RES 67 67		4-carboxyglutamate.
FT	MOD_RES 70 70		4-carboxyglutamate.
FT	MOD_RES 76 76		4-carboxyglutamate.
FT	MOD_RES 104 104		3-hydroxyaspartate (By similarity).
FT	CARBODY 186 186		N-linked (GICNAC. .) (Potential).
FT	CARBODY 244 244		N-linked (GLCNAC. .) (Potential).
FT	CONFLICT 99 99		G > V (In Ref. 2).
SQ	SEQUENCE 446 AA; 50276 MW; 2512B44A15CBC96E CRC64;		Score 127; DB 1; Length 446;
Query Match	66.1%; Best Local Similarity 59.1%; Matches 26; Conservative 1; Mismatches 17; Indels 0; Gaps 0;		Peptidase_S1.

DR	InterPro; IPR001314; Peptidase_S1A.
DR	InterPro; IPR009003; PepI_Ser_Cys.
DR	InterPro; IPR00294; VitK_dep_GLA.
DR	Pfam; PF00008; EGF; 2.
DR	Pfam; PF00089; Glu; 1.
DR	Pfam; PF00089; Trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; ECFBLOOD.	
DR	PRINTS; PR00001; GIABLOOD.
DR	SMART; SM00179; EGF_CA; 1.
DR	SMART; SM00069; GLA; 1.
DR	SMART; SM00020; TRYPSIN; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS00186; EGF_2; 2.
DR	PROSITE; PS50026; EGF_3; 1.
DR	PROSITE; PS01187; EGF_CA; 1.
DR	PROSITE; PS00011; GLA_1; 1.
DR	PROSITE; PS50998; GLA_2; 1.
DR	PROSITE; PS00134; TRYPSIN_DOMAIN; 1.
DR	PROSITE; PS00135; TRYPSIN_SEB; 1.
KW	Blood coagulation; Calcium-binding; Direct protein sequencing;
KW	EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;
KW	Plasma; Repear; Serine protease; Vitamin K; Zymogen.
PT	CHAIN 1 152 Factor VII light chain.
FT	CHAIN 153 407 Factor VII heavy chain.
FT	DOMAIN 1 45 Gla.
FT	DOMAIN 46 82 EGF-like 1, calcium-binding (Potential).
FT	DOMAIN 87 128 EGF-like 2.
FT	DOMAIN 153 407 Serine protease.
FT	SITE 152 153 Cleavage (By factor Xa, factor XIIa, factor IXa, or thrombin).
FT	ACT SITE 193 193 By similarity.
FT	ACT SITE 242 242 By similarity.
FT	ACT SITE 344 344 By similarity.
FT	BINDING 338 338 Substrate (By similarity).
FT	DISULFID 17 22 By similarity.
FT	DISULFID 50 61 By similarity.
FT	DISULFID 55 70 By similarity.
FT	DISULFID 72 81 By similarity.
FT	DISULFID 91 102 By similarity.
FT	DISULFID 98 112 By similarity.
FT	DISULFID 114 127 By similarity.
FT	DISULFID 135 262 By similarity.
FT	DISULFID 159 164 By similarity.
FT	DISULFID 178 194 By similarity.
FT	DISULFID 310 329 By similarity.
FT	DISULFID 340 368 By similarity.
FT	MOD_RES 6 6 4-carboxyglutamate.
FT	MOD_RES 7 7 4-carboxyglutamate.
FT	MOD_RES 14 14 4-carboxyglutamate.
FT	MOD_RES 16 16 4-carboxyglutamate.
FT	MOD_RES 19 19 4-carboxyglutamate.
FT	MOD_RES 20 20 4-carboxyglutamate.
FT	MOD_RES 25 25 4-carboxyglutamate.
FT	MOD_RES 26 26 4-carboxyglutamate.
FT	MOD_RES 29 29 4-carboxyglutamate.
FT	MOD_RES 35 35 4-carboxyglutamate.
FT	CARBOHYD 52 52 O-linked (Glc . . .).
FT	CARBOHYD 145 145 N-linked (GlcNAc . . .).
FT	CARBOHYD 203 203 N-linked (GlcNAc . . .).
SEQUENCE	407 AA; 44431 MW; 703E1F506367F10 CRC64;
Query Match	64.1%; Score 123; DB 1; Length 407;
Best Local Similarity	54.3%; Pred. No. 2.6e-13;
Matches 23;	Conservative 5; Mismatches 16; Indels 0; Gaps 0;
Qy	1 ANATXXLPGSLLXRXCXXQCSPXXKAXIFKDAKRTKLWISY 44
Db	1 ANGPFLEELFGSLRECREELCSFEAHBFIRNEERTQFWVNSY 44

RESULT 6	
PRTC_PIG	STANDARD:
ID_PIG	PRT;
AC_Q9GP2;	459 AA.
AC_Q9GP2;	(Rel. 40, Created)
DT_16-OCT-2001	(Rel. 40, Last sequence update)
DT_16-OCT-2001	(Rel. 40, Last annotation update)
DT_25-OCT-2004	(Rel. 45, Last annotation update)
DB_Vitamin K-dependent Protein C Precursor (BC 3.4.21.69)	(Anticoagulant protein C) (Blood coagulation factor XIV).
DE_DE	(Autoproteobmin II A) (Anticoagulant protein C) (Blood coagulation factor XIV).
DE_DE	Name=PROCF;
OS_Sus_scrofa (Pig);	Colter M.B., Braunschweig M., Alexander L.J., Neame P.J., Grimm D.R., Kim H.K.W., Kim H.K.W.;
RA_MEDLINE=21121490; PubMed=112299814;	RT_Porcine factor V; cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains;"
RA_CELL_MOL_LIFE SCI. 58:148-159(2001).	RT_RL
RA_N11 -	CC FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIa in the presence of calcium ions and phospholipids.
RA_N11 -	CC CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.
RA_N11 -	CC SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
RA_N11 -	CC TISSUE SPECIFICITY: Plasma; synthesized in the liver.
RA_N11 -	CC PTM: The vitamin K-dependent enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
RA_N11 -	CC MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Glu domain. This Glu-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
RA_N11 -	CC SIMILARITY: Belongs to the peptidase S1 family.
RA_N11 -	CC SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.
RA_N11 -	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA_N11 -	CC EMBL; AF191307; AAC28380.1; -
RA_N11 -	CC HSSP; P04070; 1AUT.
DR_MEOPS; S01_218; -	DR_MEOPS; S01_218; -
DR_InterPro; IPR001152; Asx_Hydroxyyl_S	DR_InterPro; IPR001152; Asx_Hydroxyyl_S
DR_InterPro; IPR007442; EGF_2;	DR_InterPro; IPR007442; EGF_2;
DR_InterPro; IPR001881; EGF_Ca	DR_InterPro; IPR001881; EGF_Ca
DR_InterPro; IPR00209; EGF_Like	DR_InterPro; IPR00209; EGF_Like
DR_InterPro; IPR003383; GLA_Blood	DR_InterPro; IPR003383; GLA_Blood
DR_InterPro; IPR00210; IEGF	DR_InterPro; IPR00210; IEGF
DR_InterPro; IPR00303; Pept_Ser_Cys	DR_InterPro; IPR00303; Pept_Ser_Cys
DR_InterPro; IPR001254; PeptDatabase_S1A	DR_InterPro; IPR001254; PeptDatabase_S1A
DR_InterPro; IPR001314; PeptDatabase_S1A	DR_InterPro; IPR001314; PeptDatabase_S1A
DR_InterPro; IPR00294; VitK_dep_GLA	DR_InterPro; IPR00294; VitK_dep_GLA
DR_Pfam; PF00008; EGF; 2.	DR_Pfam; PF00008; EGF; 2.
DR_Pfam; PF00594; Glu; 1.	DR_Pfam; PF00594; Glu; 1.
DR_Pfam; PF00089; Trypsin; 1	DR_Pfam; PF00089; Trypsin; 1
PRINTS; PR00722; CHYNOTRYPSIN.	PRINTS; PR00722; CHYNOTRYPSIN.

DR	PRINTS; PRO0001; GLABLOOD.	01-FEB-1994 (Rel. 28, Created)
SMART	SM00181; BGF; 2.	DT 05-JUL-2004 (Rel. 44, Last sequence update)
SMART	SM00069; GLA; 1.	DT 25-OCT-2004 (Rel. 45, Last annotation update)
SMART	SM00020; TRYPCSPC; 1.	DB Vitamin K-dependent Protein C precursor (EC 3.4.21.69)
PROSITE	PS00010; ASX_HYDROXYL; 1.	DB (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation Factor XIV).
PROSITE	PS00022; EGF_1; 1.	DB
PROSITE	PS00186; EGF_2; 2.	DB
PROSITE	PS00026; EGF_3; 1.	DB
PROSITE	PS00187; EGF_LCA; 1.	DB
PROSITE	PS00011; GLA_1; 1.	GN Name=ProC
PROSITE	PS00098; GLA_2; 1.	OS Mus musculus (Mouse)
PROSITE	PS00240; TRYPSIN_DOM; 1.	OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
PROSITE	PS00134; TRYPSIN_HIS; 1.	OC NCBI_TaxID=10090;
PROSITE	PS00135; TRYPSIN_SER; 1.	OX
Blood coagulation; Calcium-binding; BGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein domain; Hydrolase; Hydroxylation; Repeat; Serine protease; Signal; Vitamin K.		
KW	SIGNAL	[1]
PT	PROPEP	RN SEQUENCE FROM N.A.
PT	CHAIN	RP STRAIN=BALB/C; TISSUE=Liver; MEDLINE=9216887; PubMed=1618739;
PT	CHAIN	RC STRAIN=BALB/C; TISSUE=Liver; MEDLINE=9216887; PubMed=1618739;
PT	CHAIN	RA Jaldbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D., Castellino F.J.; "Isolation and characterization of a mouse protein C cDNA." J. Biochem. 111:491-495(1992).
PT	DOMAIN	[2]
PT	DOMAIN	RN SEQUENCE FROM N.A.
PT	DOMAIN	RP STRAIN=129/SvJ; MEDLINE=96152576; PubMed=9493582;
PT	DOMAIN	RC STRAIN=C57BL/6; MEDLINE=96152576; PubMed=9493582;
PT	PEPTIDE	RA Jaldbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D., Castellino F.J.; "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C." Thromb. Haemost. 79:310-316(1998).
PT	PEPTIDE	[3]
PT	SITE	RN SEQUENCE FROM N.A.
PT	SITE	RP STRAIN=C57BL/6;
PT	DOMAIN	RA Korf I.; "Complete sequence of UC72A01;" Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
PT	DOMAIN	[4]
PT	MOD_RES	RN SEQUENCE FROM N.A.
PT	MOD_RES	RP TISSUE=Liver; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/phas.242603899;
PT	MOD_RES	RC STRAUBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Schaefer C.F., Bhat N.K., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.W., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Rubin G.M., Hong L., Diatchenko L., Marsusina K., Farmer A.A., Bonaldo M.P., Casabot T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullshy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heilcon E., Kettman J., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez J., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schein J.E., Jones S.J.M., Marrs M.A., Prok Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
PT	ACT_SITE	RN SEQUENCE OF 274-433 FROM N.A.
PT	ACT_SITE	RC STRAIN=BALB/C; MEDLINE=9431874; PubMed=8033441;
PT	ACT_SITE	RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.; "A comparative study of partial primary structures of the catalytic region of mammalian protein C."
PT	DISULFID	RT RL J. Haematol. 86:590-600(1994).
PT	DISULFID	CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIa in the presence of calcium ions and phospholipids.
PT	DISULFID	CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.
PT	DISULFID	CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a
PQ	SEQUENCE	1 ANAFLXXLRPGSLRXCKXXQCSFXXXARXIPKDXAXTKLFWIWSY 44 .
Db	SEQUENCE	2 ANSPLEBLRPSSERECRETECDFEEIFONTNTMAFWNSKY 85 .

RESULT 7

PRTC_MOUSE STANDARD PRT; 460 AA.
 ID_PRTC_MOUSE STANDARD Q99PC6;
 AC P33587; O35498; Q91WN8; Q99PC6;

tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

-I- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

-I- SIMILARITY: Belongs to the Peptidase S1 family.

-I- SIMILARITY: Contains 2 EGF-like domains.

-I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR D10445; BAA01235; 1; .
 DR EMBL; AF034569; ARG33795; 1; .
 DR EMBL; AF18182; AAC07948; 1; .
 DR EMBL; BC013896; AAC013896; 1; .
 DR EMBL; D47555; BAA010812; 1; .
 DR PIR; JX010; JX0210.
 DR HSSP; P0070; IAUT.
 DR MEROPS; S01; 218; ~.
 DR MGD; MG1; 19777; PROC.
 DR InterPro; IPR00015; Asx hydroxyyl S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR00188; EGF_Ca.
 DR InterPro; IPR00620; EGF like.
 DR InterPro; IPR00238; GLA_like.
 DR InterPro; IPR00900; Pept_Ser_Cys.
 DR InterPro; IPR00125; Peptidase_S1.
 DR InterPro; IPR00134; Peptidase_SIA.
 DR InterPro; IPR000294; VitK_dep_GLAs.
 PFam; PF00008; EGF; 2.
 PFam; PF00594; Gla; 1.
 PFam; PF00089; Trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SNO0179; EGF_Ca; 1.
 DR SMART; SNO0063; GLA; 1.
 SMART; SNO0020; TRYSP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF; 1.
 DR PROSITE; PS01186; EGF; 2; 2.
 DR PROSITE; PS50026; EGF; 3; 1.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLA; 1; 1.
 DR PROSITE; PS50598; GLA; 1; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL; 1; 33; By similarity.

FT PROPEP; 34; 41; By similarity.
 FT CHAIN; 42; 460; Vitamin K-dependent protein C light chain
 (By similarity).
 FT CHAIN; 199; 460; Vitamin K-dependent protein C heavy chain
 (By similarity).
 FT PEPTIDE SITE; 199; 212; Activation Peptide (By similarity).
 FT DOMAIN; 212; 213; Cleavage (by thrombin) (By similarity).
 FT DOMAIN; 42; 87; Gla.
 FT DOMAIN; 96; 131; EGF-like 1.

CC	FT	DOMAIN	135	175	EGF-like 2.
CC	FT	DOMAIN	213	460	Serine protease.
CC	FT	MOD_RES	47	47	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	48	48	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	55	55	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	57	57	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	60	60	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	61	61	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	66	66	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	67	67	4-carboxyglutamate (By similarity).
CC	FT	MOD_RES	70	70	4-hydroxyaspartate (By similarity).
CC	FT	ACT_SITE	112	112	3-hydroxyaspartate (By similarity).
CC	FT	ACT_SITE	253	253	Charge relay system.
CC	FT	ACT_SITE	299	299	Charge relay system.
CC	FT	ACT_SITE	401	401	Charge relay system.
CC	FT	DISULFID	58	63	By similarity.
CC	FT	DISULFID	91	110	By similarity.
CC	FT	DISULFID	100	105	By similarity.
CC	FT	DISULFID	104	119	By similarity.
CC	FT	DISULFID	121	130	By similarity.
CC	FT	DISULFID	139	150	By similarity.
CC	FT	DISULFID	146	159	By similarity.
CC	FT	DISULFID	161	174	Interchain (By similarity).
CC	FT	DISULFID	182	219	By similarity.
CC	FT	DISULFID	238	254	By similarity.
CC	FT	DISULFID	372	386	By similarity.
CC	FT	DISULFID	397	425	N-linked (GICNAC . .) (Potential).
CC	FT	CARBONYD	214	214	N-linked (GICNAC . .) (Potential).
CC	FT	CARBONYD	290	290	N-linked (GICNAC . .) (Potential).
CC	FT	CARBONYD	354	354	N-linked (GICNAC . .) (Potential).
CC	FT	VARIANT	327	327	Q > Q (in strain BALB/c).
CC	FT	VARIANT	392	392	D > N (in strain BALB/c).
CC	FT	CONFLICT	65	65	F > L (in Ref. 3).
CC	SQ	SEQUENCE	460	51818 MW;	01172668FCC274 CRC64;
CC	Query Match Best Local Similarity Matches 21; Conservative 5; Mismatches 18; Indels 0; Gaps 0;				
CC	Score 109; DB 1; Length 460;				
CC	Pred. No. 1e-10; Pred. No. 1e-10;				
CC	Matches 21; Conservation 5; Mismatches 18; Indels 0; Gaps 0;				
CC	Qy	1	ANAFLXXLRPGSLXRKCKXQCSFXKXKIFDAXTKFLKFLNSY 44		
CC	Db	42	ANSPLLEMNRPGSLEREEMEEICDPEEEAQEEIQNFVNDTLAFWIKY 85		
RESULT 8					
CC	FA7_RAT	STANDARD;	PRT;	446 AA.	
CC	ID FA7_RAT	OBK306;			
CC	AC	OBK306;			
CC	DT	05-JUL-2004 (Rel. 44, Created)			
CC	DT	05-JUL-2004 (Rel. 44, Last sequence update)			
CC	DT	25-OCT-2004 (Rel. 45, Last annotation update)			
CC	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).				
CC	GN	Name=FA7;			
CC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratius.				
CC	OC	OC			
CC	RN [1]	NCBI TAXID=10116;			
CC	RP	SEQUENCE FROM N.A.			
CC	RC	STRAIN-Sprague-Dawley;			
CC	RA	Murphy K., Ramaker M.;			
CC	RT	"Nucleotide sequence of the cDNA encoding rat coagulation factor VII."			
CC	RT	Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases			
CC	-!-	FUNCTION: Initiates the extrinsic pathway of blood coagulation.			
CC	Seine protease that circulates in the blood in a zymogen form.				
CC	Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor Xa by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium (By similarity).				

CC	- I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to form factor Xa.	FT	DISU9FID	96	111	By similarity.
CC	- I- SUBUNIT: Retrodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).	FT	DISU9FID	113	122	By similarity.
CC	- I- TISSUE SPECIFICITY: Plasma.	FT	DISU9FID	132	143	By similarity.
CC	- I- PIM: the vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).	FT	DISU9FID	139	153	By similarity.
CC	- I- SIMILARITY: Belongs to the peptidase S1 family.	FT	DISU9FID	155	168	By similarity.
CC	- I- SIMILARITY: Contains 2 EGF-like domains.	FT	DISU9FID	176	303	By similarity.
CC	- I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.	FT	DISU9FID	200	205	By similarity.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	DISU9FID	219	235	By similarity.
CC	HSSP: P08709; 1KLJ.	FT	DISU9FID	351	370	By similarity.
DR	RGD: 628678; P7.	FT	DISU9FID	381	409	By similarity.
DR	InterPro: IPR000086; Aldehyde dehydrogenyl S.	FT	MODRES	47	47	4-carboxyglutamate (By similarity).
DR	InterPro: IPR000152; Asx_hydroxyl_S.	FT	MODRES	48	48	4-carboxyglutamate (By similarity).
DR	InterPro: IPR000742; EGF_1.	FT	MODRES	55	55	4-carboxyglutamate (By similarity).
DR	InterPro: IPR000881; EGF_Ca.	FT	MODRES	57	57	4-carboxyglutamate (By similarity).
DR	InterPro: IPR001438; EGF_I1.	FT	MODRES	60	60	4-carboxyglutamate (By similarity).
DR	InterPro: IPR006209; EGF_Ilike.	FT	MODRES	61	61	4-carboxyglutamate (By similarity).
DR	InterPro: IPR002383; GLA_blood.	FT	MODRES	66	66	4-carboxyglutamate (By similarity).
DR	InterPro: IPR001254; PepFidase_S1.	FT	MODRES	67	67	4-carboxyglutamate (By similarity).
DR	InterPro: IPR013144; Peptidase_S1A.	FT	MODRES	70	70	4-carboxyglutamate (By similarity).
DR	InterPro: IPR003003; Pept_Ser_Cys.	FT	MODRES	76	76	4-carboxyglutamate (By similarity).
DR	InterPro: IPR000294; VitK_dep_GLA.	FT	CARBHYD	104	104	3-hydroxyaspartate (By similarity).
DR	Pfam: PF00000; EGF_2.	FT	CARBHYD	186	186	N-linked (GlcNAc . .) (Potential).
DR	Pfam: PF00594; Gla_1.	FT	CARBHYD	244	244	N-linked (GlcNAc . .) (Potential).
DR	PRINTS: PRO00089; Trypsin_1.	SQ	SEQUENCE	446	AA:	50399 MW;
DR	PRINTS: PRO0722; CHYMOTRYPsin.	SQ	SEQUENCE	446	AA:	292985EBF119C0AA CRC64;
RESULT 9						
		PRTC_BOVIN	Score	104;	DB 1;	Length 446;
		ID	Best Local Similarity	50.0 %;	Pred. No.	7.8E-10;
		PRTC_BOVIN	Matches	22;	Mismatches	20;
		AC	Conservative	2;	Indels	0;
		P00745;	Gaps	0;		
Qy	1 ANAFLXXLRLPGSLRXRXQCSFXXARXIPKDXAXTRKLFWIISY 44	DT	21-JUL-1986	(Rel. 01, Created)		
Db	42 ANSLLBELWSSSLERCNBRCCSPPEARETFKSPEARTQFWTIY 85	DT	13-AUG-1987	(Rel. 05, Last sequence update)		
		DB	25-OCT-2004	(Rel. 45, Last annotation update)		
		DB	Vitamin K-dependent protein C precursor (EC 3.4.21.69)	(Autoprothrombin LIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)		
		DE	Name=PROC;			
		OS	Bos taurus (Bovine).			
		OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
		OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
		OC	Bovinae; Bos.			
		NCBI_TaxID=9913;	OX			
		RN	SEQUENCE FROM N.A.			
		RX	MEDLINE=85014826; PubMed=6091100;			
		RA	Long G.L., Balagaje R.M., McGillivray R.T.A.;			
		RA	"Cloning and sequencing of liver cDNA coding for bovine protein C."			
		RT	Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).			
		RN	[2]			
		RP	SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.			
		RX	MEDLINE=83007325; PubMed=6896876;			
		RA	Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;			
		RA	"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";			
		RT	Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).			
		RL	J. Biol. Chem. 257:12170-12179(1982).			
		RN	[3]			
		RP	SEQUENCE TO 110.			
		RX	MEDLINE=83169769; PubMed=6572939;			
		RA	Stenflo J., Fernlund P., Roepstorff P., Stenflo J.;			
		RA	"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";			
		RT	Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).			
		RN	[4]			
		RP	SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-269;			
		RX	MEDLINE=B-3007326; PubMed=6896877;			
		RA	Stenflo J., Fernlund P.;			
FT	ACT_SITE 234	RA				
FT	ACT_SITE 283					
FT	ACT_SITE 385					
FT	BINDING 379					
FT	DISULPID 58					
FT	DISU9FID 91					

"Amino acid sequence of the heavy chain of bovine protein C." ;
[5] J. Biol. Chem. 257:12180-12190 (1982).

PROCESSING, AND CALCIUM-BINDING DATA.
MEDLINE-83213514; PubMed-6406503;

Johnson A.E.; Esmon N.L.; Lau T.M.; Esmon C.T.;
DeBault L.E.; Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless protein C";
J. Biol. Chem. 258:5548-5553 (1983).

[6] PROCESSING, AND CALCIUM-BINDING DATA.
MEDLINE-83213514; PubMed-6406503;

Johnson A.E.; Esmon N.L.; Lau T.M.; Esmon C.T.;
"Structural changes required for activation of protein C are induced by Ca²⁺-binding at a high affinity site that does not contain gamma-carboxyglutamic acid." ;
J. Biol. Chem. 258:5554-5560 (1983).

-1- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

-1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

-1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-1- PM: The vitamin K-dependent, enzymatic carboxylation of some Gl residues allows the modified protein to bind calcium.

-1- MISCELLANEOUS: Calcium also binds with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

-1- SIMILARITY: Belongs to the peptidase S1 family.

-1- SIMILARITY: Contains 2 EGF-like domains.

-1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Use by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/ann>) or send an email to license@isb-sib.ch.

EMBL; K02435; AAA30685.1; - .
PIR; A26250; KX00.
HSSP; P04070; IAUT.
MEROPS; S01_218; - .
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00142; BGF_C.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR006210; IEGF.
InterPro; IPR00003; Pept_Ser_Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00094; EGF; 1.
Pfam; PF00089; Trypsin; 1.
PRINTS; PRO0722; CHYNOTRIPSIN.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00181; EGF; 2.
SMART; SM00069; GLA; 1.
SMART; SM00020; TRYD_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS01886; EGF; 2.
PROSITE; PS01887; EGF; 1.
PROSITE; PS01888; EGF; 2.

DT	05-JUL-2004 (TrEMBLref). 27, Last annotation update.	
DE	Coagulation factor VIII.	
GN	Name=F8;	
OS	Brachydanio rerio (Zebrafish) (Danio rerio).	
OC	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X.";	
NCBI_TaxID	7955;	
RN		
RP	SEQUENCE FROM N.A.	
RA	"Comprehensive analysis of blood coagulation pathways in Teleostei: Evolution of coagulation factor genes and identification of zebrafish Factor VIII";	
RT	Blood Cells Mol. Dis. 0:0-0 (2002).	
RL	-1 SIMILARITY: Belongs to Peptidase family S1.	
CC	-1 SIMILARITY: Contains 1 EGF-like domain.	
DR	EMBL; AF319546; AAC8342.1; -.	
DR	HSSP; P00740; 1CFH.	
DR	ZFIN; ZDB-GENE-021206-10; f7i.	
DR	GO; GO:000576; C:extracellular; IEA.	
DR	GO; GO:0005509; F:calcium ion binding; IEA.	
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.	
DR	GO; GO:0008233; F:peptidase activity; IEA.	
DR	GO; GO:0004295; F:trypsin activity; IEA.	
DR	GO; GO:0005508; P:proteolysis and peptidolysis; IEA.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR002383; GLA_Blood.	
DR	InterPro; IPR006210; IEGF.	
DR	InterPro; IPR001254; Peptidase_S1.	
DR	InterPro; IPR001314; Peptidase_S1A.	
DR	InterPro; IPR009003; Pept_Ser_Cys.	
DR	InterPro; IPR000294; VitK_dep_GLA.	
DR	Pfam; PF00594; EGF_1.	
DR	Pfam; PF00594; Gla_1.	
DR	PRINTS; PRO0722; CHYMOTRYPSIN.	
DR	PRINTS; PRO0001; GLABLOOD.	
DR	SMART; SM00181; EGF_2.	
DR	SMART; SM00059; GLA_1.	
DR	SMART; SM00020; TRY_SPC_1.	
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.	
DR	PROSITE; PS01186; EGF_2;	
DR	PROSITE; PS00026; EGF_3; 1.	
DR	PROSITE; PS00011; GLA_1; 1.	
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	
KW	EGF-like domain; Hydrolase; Protease; Serine protease.	
SEQUENCE	443 AA; 48823 MW; 2D250471AAE94F4 CRC64;	
Query Match	53.1%; Score 102; DB 2; Length 443;	
Best Local Similarity	41.9%; Pred. No. 1.8e-09;	
Matches	18; Conservative B; Mismatches 17; Indels 0; Gaps 0;	
SQ		
Qy	2 NAFLXXLRPGSLXRCXXXCSFXXARXIFDAXRTKLNFNTSY 44	
Db	40 SGFLEEMKAGNLRECREVIECDYEEAREVTFDDDRTKQFLNSY 82	
RESULT 11		
PA10_HUMAN	STANDARD; PRT; 488 AA.	
ID	FA10_HUMAN	
AC	P00742; Q14340;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	25-JAN-2005 (Rel. 46, Last annotation update)	
DT	Coagulation factor X precursor (EC 3.4.21.6) (Stuart-Power factor).	
DB	Name=F10;	
GN	Homo sapiens (Human).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 TISSUE-Liver;
 MEDLINE=41222026; PubMed=6587384;
 Leyteus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W.;
 "Characterization of a cDNA coding for human factor X.";
 Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 [9]

RN
 SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 MEDLINE=14062825; PubMed=8223461;
 RX
 Inoue K., Morita T.;
 RT
 "Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moieties in the activation of factor X.";
 RL
 "Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.";
 RN
 SEQUENCE OF 1-23 FROM N.A.
 RX
 MEDLINE=2612918; PubMed=90529-5;
 RA
 Jagadeeswaran P., Reddy S.V., Rao K.J., Hansabhuhanam K., Lyman G.;
 RT
 "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL
 J. Mol. Biol. 232:947-966(1993).
 RN
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX
 MEDLINE=33360277; PubMed=8355279;
 RA
 Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 Huber R., Blankenship D.T., Gardin A.D., Kisiel W.;
 RT
 "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL
 J. Mol. Biol. 232:947-966(1993).
 RN
 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX
 MEDLINE=38238982; PubMed=9618463; DOI=10.1073/pnas.95.12.6630;
 RA
 Kamata K., Kawamoto H., Honma T., Iwana T., Kim S.H.;
 RT
 "Structural basis for chemical inhibition of human blood coagulation factor Xa.";
 RT
 Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 RN
 VARIANTS ILE-7 AND HIS-30.
 RX
 MEDLINE=9318093; PubMed=10391209;
 RA
 Cargill M., Altshuler D., Ireland J., Sklar P., Ardie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RT
 "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
 RT
 Nat. Genet. 22:231-238(1999).
 RN
 . [14]
 RP
 PubMed=10545957;
 RA
 Cargill M., Altshuler D., Ireland J., Sklar P., Ardie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RA
 Nat. Genet. 23:373-373(1999).
 CC
 -|- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va,
 CC
 calcium and phospholipid during blood clotting.
 CC
 -|- ARG-ILE bonds in prothrombin to form thrombin.
 CC
 -|- SUBUNIT: The two chains are formed from single chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.
 CC
 -|- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC
 -|- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.
 CC
 -|- PTM: N- and O-glycosylated.
 CC
 -|- PTM: The activation peptide is cleaved by factor IXa (in the extrinsic pathway), or by factor VIIa (in the intrinsic pathway).
 CC
 -|- SIMILARITY: Belongs to the peptide S1 family.
 CC
 -|- SIMILARITY: Contains 2 EGF-like domains.
 CC
 -|- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC
 This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR
 EMBL; K03194; AAAS2490.1;
 DR
 EMBL; M57285; AAAS242.1;
 DR
 EMBL; AF503510; AAM13147.1;
 DR
 EMBL; BC046125; AAH46125.1;
 DR
 EMBL; L29433; AAAS2764.1;
 DR
 EMBL; L00390; AAAS2764.1;
 DR
 EMBL; L00391; AAAS2764.1;
 DR
 EMBL; L00392; AAAS2764.1;
 DR
 EMBL; L00393; AAAS2764.1;
 DR
 EMBL; L00394; AAAS2764.1;
 DR
 EMBL; L00395; AAAS2764.1;
 DR
 EMBL; L00396; AAAS2764.1;
 DR
 EMBL; M22613; AAAS1984.1;
 DR
 EMBL; K01886; AAAS2486.1;
 DR
 EMBL; M33297; AAAS2636.1;
 DR
 FIR; A24478; EXPD;
 DR
 PDB; 1C5M; X-ray; D=235-488, F=84-179.
 DR
 PDB; 1E7Q; X-ray; A=235-488, B=46-179.
 DR
 PDB; 1F0R; X-ray; A=235-488, B=46-179.
 DR
 PDB; 1F0S; X-ray; A=235-488, B=46-179.
 DR
 PDB; 1FAX; X-ray; A=235-488, L=84-179.
 DR
 PDB; 1FJ5; X-ray; A=235-488, L=127-178.
 DR
 PDB; 1G2L; X-ray; A=235-469, B=86-179.
 DR
 PDB; 1H2M; X-ray; A=235-475, B=129-179.
 DR
 PDB; 1HCG; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0E; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0F; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0G; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0H; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0J; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0K; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0L; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0M; X-ray; A=235-469, L=84-179.
 DR
 PDB; 1I0N; X-ray; A=235-469, L=84-179.

Query Match 53.1%; Score 102; DB 1; Length 488;
 Best Local Similarity 40.9%; Pred. No. 2e-09;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY
 1 ANAFLXXLRPGSLXRXCXQQCSFXXARXIFCDAXPRLKLFWISY 44
 Db
 41 ANSFLEMKKKGHLERECMEETCSYEAREVFDSKTNEFWKY 84

RESULT 12
 Q804X7
 ID Q804X7 PRELIMINARY;
 AC Q804X7;
 DT 01-JUN-2003 (TRIMBLRE. 24, Created)
 DT 01-JUN-2003 (TRIMBLRE. 24, Last sequence update)
 DT 01-MAR-2004 (TRIMBLRE. 26, Last annotation update)
 DE Coagulation Factor VII (EC 3.4.21.21).
 OS Gallus gallus (Chicken).
 OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Aves; Neognathae; Galliformes; Phasianidae; Gallinidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
 CC |- SIMILARITY: Belongs to peptidase family S1.

CC	-1- SIMILARITY: Contains 1 EGF-like domain.
DR	EMBL; AF465268; AAO33363.1; -.
DR	HSSP; P08709; IKLJ.
DR	MEROPS; S01.215; -.
DR	GO; GO:000576; C:extracellular; IBA.
DR	GO; GO:000509; F:calcium ion binding; IBA.
DR	GO; GO:0004263; F:chymotrypsin activity; IBA.
DR	GO; GO:0003802; F:coagulation factor VIIa activity; IBA.
DR	GO; GO:0008233; F:peptidase activity; IBA.
DR	GO; GO:000295; F:trypsin activity; IBA.
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IBA.
InterPro	IPR000152; ABX_hydroxy1_S.
InterPro	IPR000742; EGF_2.
DR	InterPro; IPR001881; EGF_Ca.
InterPro	IPR001438; EGF_I.
DR	InterPro; IPR006209; EGF like.
DR	InterPro; IPR002383; GLA_blood.
DR	InterPro; IPR006110; EGF_1.
DR	InterPro; IPR001254; Peptidase_S1.
DR	InterPro; IPR001314; Peptidase_S1A.
DR	InterPro; IPR009003; Pept_Ser_Cys.
InterPro	IPR000294; VitK_dep_GLA.
DR	PFam; PF00008; EGF_1.
DR	PFam; PF00594; G1a_1.
DR	PRINTS; PS00722; CHYMOTRYPsin.
DR	PRINTS; PRO0010; EGFBLOOD.
DR	SMART; SM00181; EGF_2.
DR	SMART; SM0069; GLA_1.
DR	SMART; SM0020; TRYSPC_1.
DR	PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS50026; EGF_3; 1.
DR	PROSITE; PS01187; EGF_CA; 1.
DR	PROSITE; PS00011; GLA_1; 1.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00144; TRYPSIN_HIS; UNKNOWN_1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	EGF-like domain; Hydrolase; Protease; Serine protease.
SQ	SEQUENCE 425 AA; 47626 MW; 36A9BF0DB8C6D4 CRC64;
Qy	1 ANAFLXXLRPGSSLXRXCKXQCSFXXXKFKDAXRTKLWISY 44
Db	41 ANSFPEEIKGLPPLERECIEKCSFEEARFYRDDERTKEWHY 84
RESULt 13	FA10_BOVIN
ID	STANDARD;
AC	P00743; 01, Created
DT	21-JUL-1996 (Rel. 01, Last sequence update)
DT	25-JAN-2005 (Rel. 46, Last annotation update)
DE	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN	Bos taurus (Bovine)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovirnae; Bos.
OX	NCBI_TAXID:9913;
RN	SEQUENCE OF 1-487 FROM N.A. MEDLINE=84247315; PubMed=6330671;
RX	Fung M.R., Campbell R.M., McGillivray R.T.A.; "Blood coagulation factor X mRNA encodes a single polypeptide chain containing a prepro leader sequence." Nucleic Acids Res. 12:4481-4492(1984);

RA Telemann O.; "Three-dimensional structure of the apo form of the N-terminal EGF-like module of blood coagulation factor X as determined by NMR spectroscopy and simulated folding.", *J. Biomol. Spectrosc.* 31:594-598 (1992). [12]

RT STRUCTURE BY NMR OF 85-126.

RX MEDLINE=2406322; Pubmed=1520704; DOI=10.1021/bi960633j;

RA Stenflo J., Drakenberg T.; "How an epidermal growth factor (EGF)-like domain binds calcium. High resolution NMR structure of the calcium form of the NH2-terminal EGF-like domain in coagulation factor X.", *J. Biol. Chem.* 267:19642-19649 (1992). [13]

RP STRUCTURE BY NMR OF 41-126.

RX MEDLINE=96387194; Pubmed=8794734; DOI=10.1021/bi960633j;

RA Sunnerhaugen M., Olah G.A., Stenflo J., Forseen S., Drakenberg T., Trehella J.; "The relative orientation of Glu and EGF domains in coagulation factor X is altered by Ca²⁺ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.", *Biochemistry* 35:11547-11559 (1996).

CC -!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of Factor Va, calcium and phospholipid during blood clotting.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-| -Thr and then Arg-| -Ile bonds in prothrombin to form thrombin.

CC -!- SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.

CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.

CC -!- PTM: N- and O-Glycosylated.

CC -!- PTM: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or by factor VIIa (in the extrinsic pathway).

CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Glu domain.

CC -!- SIMILARITY: Belongs to the peptidase S1 family.

CC -!- SIMILARITY: Contains 2 EGF-like domains.

CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce> or send an email to license@isb-sib.ch).

CC EMBL: X00673; CAA252286.1; -.

DR PIR; A22867; EXBO.

DR PDB; 1APO; NMR; @=05-126.

DR PDB; 1IOD; X-ray; G=41-84.

DR PDB; 1KIG; X-ray; H=234-474, L=129-179.

DR MEROPS; S01_216; -.

DR GlycoSuiteDB; P00743; -.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR000742; EGFr2.

DR PROSITE; PS00001; GLABLOOD.

DR PROSITE; PS000010; ASX_HYDROXYL; 1.

DR PROSITE; PS000022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS50026; EGF_3; 1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS50011; GLA_1; 1.

DR PROSITE; PS50998; GLA_2; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW 3D-structure: Blood coagulation: Calcium-binding;

KW Direct protein sequencing; EGF-like domain;

KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolyase; Hydroxylation;

KW Plasma; Repeat; Serine protease; Signal; Sulfation; Vitamine K;

KW Zymogen.

KW Potential.

FT SIGNAL 1 23

FT PROPEP 24 40

FT CHAIN 41 492

FT CHAIN 41 492

FT PROPEP 183 492

FT PROPEP 183 233

FT CHAIN 234 492

FT PROPEP 476 492

FT DOMAIN 41 85

FT DOMAIN 86 122

FT DOMAIN 125 165

FT DOMAIN 234 492

FT SITE 233 234

FT ACT SITE 275 275

FT ACT SITE 321 321

FT ACT SITE 418 418

Query Match 52.6%; Score 101; DB 1; Length 492;

Best Local Similarity 43.2%; Pred. No. 3e-09; 18; Indels 0; Gaps 0;

Matches 19; Conservative 7; Mismatches 18;

Qy 1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXKIFDKXPKLFWIYSY 44

Db 41 ANSFLEEVTKQNLRECLLEACSLEEAREVFEDAEQDEFWNSKY 84

RESULT 14

PRTC_RAT STANDARD; PRT; 461 AA.

ID P31394; AC P31394; DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Vitamin K-dependent protein C precursor (EC 3.4.21.69) (Anticoagulant protein C) (Blood coagulation factor XIV).

GN Name=Proc; OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116; [1]

RN Sequence from N.A.

RP STRAIN=Mistar; TISSUE=Liver;

RC MEDLINE=92339550; Published=1627650; DOI=10.1016/0167-4781(92)90035-X;

RX Okaishi T., Maekawa K., Nawa K., Marumoto Y.; "The cDNA cloning and mRNA expression of rat protein C.";

RT Blochim. Biophys. Acta 1131:329-332 (1992).

CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.

CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved

into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-I- PM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

-I- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Gla domain. This Gla-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

-I- SIMILARITY: Belongs to the Peptidase S1 family.

-I- SIMILARITY: Contains 2 EGF-like domains.

-I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/>, or send an email to license@isb-sib.ch).

DR EMBL: X64136; CAA45617.1; -.

DR PIR: S18994; S18994.

DR MEROPS: S01_218; -.

DR RGD: 3411; Proc.

DR InterPro: IPR000152; Asx_hydroxyl_S.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR006209; EGF_Like.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR009003; pepF_Ser_Cys.

DR InterPro: IPR001254; Peptidase_S1.

DR InterPro: IPR001314; Peptidase_S1A.

DR InterPro: IPR000294; VitK_dep_Gla.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; Gla_1.

DR Pfam: PF00009; Trypsin; 1.

DR PRINTS: PR000722; CHMOTRTPSIN.

DR SMART: SM000020; SPC_1.

DR PROSITE: PS00010; ASX_HYDROXYL_1.

DR SMART: SM00069; GLA_1.

DR PROSITE: SM00020; TRYPSIN DOM_1.

DR PROSITE: PS00010; ASX_HYDROXYL_1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS00186; EGF_2; 2.

DR PROSITE: PS00036; EGF_3; 1.

DR PROSITE: PS00011; Gla_1; 1.

DR PROSITE: PS00098; Gla_2; 1.

DR PROSITE: PS00011; TRYPSIN HIS_1.

DR PROSITE: PS00020; TRYPSIN DOM_1.

DR PROSITE: PS000134; TRYPSIN SER_1.

KW PROTEIN DOMAIN: Calcium-binding; EGF-like domain; Hydrolase; Glycoprotein; Hydrolase; Hydroxylation; Repeate; Serine protease; Signal; Vitamin K.

KW PROTEIN DOMAIN: Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation; Repeate; Serine protease; Signal; Vitamin K.

FT PROPEP SIGNAL 1 32 By similarity.

FT PROPEP CHAIN 42 41 Vitamin K-dependent protein C light chain

FT PROPEP CHAIN 42 196 Vitamin K-dependent protein C light chain

FT PROPEP CHAIN 199 461 Vitamin K-dependent protein C heavy chain

FT PEPTIDE DOMAIN 42 87 Activation peptide (By similarity).

FT PEPTIDE DOMAIN 96 131 EGF-like 1.

FT PEPTIDE DOMAIN 135 175 EGF-like 2.

FT PEPTIDE DOMAIN 213 461 Serine protease.

FT SITE 212 Cleavage (by thrombin) (By similarity).

CC MOD_RES 47 47 4-carboxyglutamate (By similarity).

CC MOD_RES 48 48 4-carboxyglutamate (By similarity).

CC MOD_RES 55 55 4-carboxyglutamate (By similarity).

CC MOD_RES 57 57 4-carboxyglutamate (By similarity).

CC MOD_RES 60 60 4-carboxyglutamate (By similarity).

CC MOD_RES 61 61 4-carboxyglutamate (By similarity).

CC MOD_RES 66 66 4-carboxyglutamate (By similarity).

CC MOD_RES 67 67 4-carboxyglutamate (By similarity).

CC MOD_RES 70 70 4-carboxyglutamate (By similarity).

FT MOD_RES 112 112 3-hydroxyaspartate (By similarity).

FT ACT_SITE 254 254 Charge relay system.

FT ACT_SITE 300 300 Charge relay system.

FT ACT_SITE 402 402 Charge relay system.

FT DISUFID 58 63 By similarity.

FT DISUFID 91 110 By similarity.

FT DISUFID 100 105 By similarity.

FT DISUFID 104 119 By similarity.

FT DISUFID 121 130 By similarity.

FT DISUFID 139 150 By similarity.

FT DISUFID 146 159 By similarity.

FT DISUFID 161 174 By similarity.

FT DISUFID 182 320 By similarity.

FT DISUFID 239 255 By similarity.

FT DISUFID 373 387 By similarity.

FT DISUFID 398 426 By similarity.

FT CAREHYD 215 215 N-linked (GlcNAc . .) (Potential).

FT CAREHYD 291 291 N-linked (GlcNAc . .) (Potential).

FT CAREHYD 355 355 N-linked (GlcNAc . .) (Potential).

FT SQ 51912 MW; 8A4C93664EDACD5 CRC64;

SEQUENCE 461 AA; SQ

Query Match 52.1%; Score 100; DB 1; Length 461;

Best Local Similarity 45.5%; Pred. No. 4.3e-09;

Matches 20; Conservative 5; Mismatches 19; Indels 8 0; Gaps 0;

OS Rattus norvegicus (Rat).

GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RESULT 15

Q68PF8 068PF8 PRELIMINARY; PRT; 461 AA.

ID Q68PF8 ID Q68PF8 PRELIMINARY; PRT; 461 AA.

AC Q68PF8; AC Q68PF8; PRELIMINARY; PRT; 461 AA.

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE Protein C.

GN Name=Proc;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116; OX [1]

RN RN SEQUENCE FROM N.A.

RC TISSUE=Lung; RC TISSUE=Lung; DOI=10.1073/pnas.242603899; PMID=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaeffer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquai Lano N.A., Peters G.J., Abramson K.J., Malek J.A., Gunaratne P.H., Bosak S.A., McEwan P.J., McBernan K.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalba D.K., Muny E.J., Lu X., Sodergren E.J., Gibbs R.A., Fahay J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimm J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimm J., Schmutz J., Smailus D.B., Schnurch A., Krzywinski M.I., Skalska U., Schein J.E., Jones S.J., Marrs M.A., RA

"Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]

SEQUENCE FROM N.A.

RN TISSUE=Lung;
 RP Director MGC Project;
 RC Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 DR EMBL; BC078879; AAH78879.1; .
 DR InterPro; IPR000152; ABX_hydroxy_S.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR00383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR009003; Pept Ser_Cys.
 DR InterPro; IPR000294; VitK_dep_GLA.
 PFam; PF00008; EGF; 1.
 PFam; PF00594; Gla; 1.
 PFam; PF00089; Trypsin; 1.
 PRINTS; PRO0722; CHIMOTRYPsin.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00181; EGF; 2.
 SMART; SM01179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00020; TRYD_SPC; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; UNKNOWN_1.
 PROSITE; PS01186; EGF_2; 2.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLA_1; UNKNOWN_1.
 PROSITE; PS50240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HTS; UNKNOWN_1.
 PROSITE; PS00135; TRYPSIN_SEP; 1.
 KW Hydrolase; Protease; Serine_protease.
 SEQUENCE 461 AA; 51826 MN; C0181CED046B584B CRC64;

Query Match 52.1%; Score 100; DB 2; Length 461;
 Best Local Similarity 45.5%; Pred. No. 4.3e-09;
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 ANAFLXXLRGSILRXCXXQCSFXXARYLFKDAXRTKLFWISY 44
 Db 42 ANSFLEEVRAGSLERCMEEICDPPEAQEFQNVDTLAFWIKY 85

Search completed: August 22, 2005, 09:36:14
 Job time : 176 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	172	89.6	44	3 US-08-955-536-3	Sequence 3, Appli
2	172	89.6	44	4 US-09-203-239-3	Sequence 3, Appli
3	172	89.6	44	4 US-09-197-531-3	Sequence 3, Appli
4	172	89.6	44	4 US-09-190-810-3	Sequence 3, Appli
5	172	89.6	406	1 US-08-293-778-24	Sequence 24, Appli
6	172	89.6	406	1 US-08-395-411-5	Sequence 5, Appli
7	172	89.6	406	2 US-08-955-417-1	Sequence 5, Appli
8	172	89.6	406	4 US-09-781-587B-1	Sequence 1, Appli
9	172	89.6	406	4 US-09-782-587B-3	Sequence 3, Appli
10	172	89.6	406	5 PCT-US92-10242-5	Sequence 5, Appli
11	172	89.6	444	1 US-08-475-845-2	Sequence 2, Appli
12	172	89.6	444	2 US-08-127-630-2	Sequence 2, Appli
13	172	89.6	444	2 US-08-160-889-2	Sequence 2, Appli
14	172	89.6	444	2 US-08-537-807-2	Sequence 2, Appli
15	172	89.6	444	2 US-08-371-003-2	Sequence 2, Appli
16	172	89.6	444	3 US-08-464-333-2	Sequence 2, Appli
17	172	89.6	444	3 US-09-189-607-2	Sequence 2, Appli
18	172	89.6	444	3 US-09-378-907-2	Sequence 2, Appli
19	172	89.6	444	5 PCT-US94-05779-2	Sequence 2, Appli
20	172	89.6	461	4 US-09-949-016-8839	Sequence 8839, Appli
21	172	89.6	466	1 US-07-882-202A-4	Sequence 4, Appli
22	172	89.6	466	1 US-08-021-615A-4	Sequence 4, Appli
23	172	89.6	466	1 US-08-321-777-4	Sequence 4, Appli
24	172	89.6	466	3 US-09-009-227-14	Sequence 14, Appli
25	172	89.6	466	3 US-09-009-656-14	Sequence 14, Appli
26	172	89.6	466	5 PCT-US93-04493-4	Sequence 4, Appli
27	172	89.6	483	4 US-09-949-016-9523	Sequence 9523, Appli

NAME/KEY : MOD_RES
 LOCATION : (0)...(0)
 OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-09-3102-239-3

Query Match 89.6%; Score 172; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1e-21;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLRXCXXQCSPXXARXIFKDAKRTKLFWISY 44
 Db 1 ANAFLXXLRPGSLRXCXXQCSPXXARXIFKDAKRTKLFWISY 44

RESULT 5
 US-08-293-778-24 ; Sequence 24, Application US/08293778
 Patent No. 550560

GENERAL INFORMATION:
 / APPLICANT: Nicolaisen, Else M.
 / APPLICANT: Bjorn, Soren E.
 / APPLICANT: Wiberg, Finn C.
 / APPLICANT: Goodbury, Richard
 / TITLE OF INVENTION: MODIFIED FACTOR VII/VIIa
 / NUMBER OF SEQUENCES: 26
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: No. 550560 No. 5580560disk of No. 5580560th America, Inc.
 / STREET: 405 Lexington Avenue, 62nd Floor
 / CITY: New York
 / STATE: New York
 / COUNTRY: United States of America
 / ZIP: 10174-6201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/293,778
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/104,509
 FILING DATE:
 APPLICATION NUMBER: DK 3235/87
 FILING DATE: 25-JUN-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/434,149
 FILING DATE: 13-NOV-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK88/00103
 FILING DATE: 24-JUN-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/898,248
 FILING DATE: 12-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Agris, Cheryl H.
 REGISTRATION NUMBER: 3129-224-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 406 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-293-778-24

Query Match 89.6%; Score 172; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 1e-21;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLRXCXXQCSPXXARXIFKDAKRTKLFWISY 44
 Db 1 ANAFLXXLRPGSLRXCXXQCSPXXARXIFKDAKRTKLFWISY 44

RESULT 4
 US-09-803-810-3 ; Sequence 3, Application US/09803810
 Patent No. 676286

GENERAL INFORMATION:
 / APPLICANT: NeJsestuen, Gary L.
 / TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
 / POLYPEPTIDES
 / FILE REFERENCE: 09331/002001
 CURRENT APPLICATION NUMBER: US/09/803,810
 CURRENT FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 44

TYPE: PPT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY : MOD_RES
 LOCATION : (0)...(0)
 OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

US-09-803-810-3

RESULT 6
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639

GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods for Inhibiting Coagulation
TITLE OF INVENTION: Anti-Peptide Antibodies
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REREFERENCE/DOCKET NUMBER: TSR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"

FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match Score 89.6%; Length 406;
Best Local Similarity 77.3%; Pred. No. 1e-20;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
RESULT 8
US-09-782-587B-1

; Sequence 1, Application US/09782587B
; Patent No. 6806063
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAE, CLAUS
; APPLICANT: BORNAE, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26

RESULT 7
US-08-955-171-5
Sequence 5, Application US/08955471
Patent No. 5988751
GENERAL INFORMATION:

PRIOR APPLICATION NUMBER: PA 2000 00218
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 60/184,036
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/241,916
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 406
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (6) - (7)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (14)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (16)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (19) - (20)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (25) - (26)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (29)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (35)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

US-09-782-587B-1

Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 100.0%; Pred. No. 1e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRLPGSLXRXCXQCSFXXARYKFDAXRKLFWIISY 44
 Db 1 ANAFLXXLRLPGSLXRXCXQCSFXXARYKFDAXRKLFWIISY 44

RESULT 9

US-09-782-587B-3

Sequence 3, Application US/09782587B
 Patent No. 6806063
 GENERAL INFORMATION:
 APPLICANT: PEDERSEN, ANDERS H.
 APPLICANT: ANDERSON, KIM V.
 APPLICANT: BORNAS, CLAUS
 TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
 FILE REFERENCE: 31-001100US
 CURRENT APPLICATION NUMBER: US/09/782,587B
 CURRENT FILING DATE: 2002-03-26
 PRIOR APPLICATION NUMBER: PA 2000 00218
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 60/184,036
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/241,916
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3
 LENGTH: 406
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-782-587B-3

Query Match 89.6%; Score 172; DB 4; Length 406;
 Best Local Similarity 77.3%; Pred. No. 1e-20;
 Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRLPGSLXRXCXQCSFXXARYKFDAXRKLFWIISY 44
 Db 1 ANAFLXXLRLPGSLXRXCXQCSFXXARYKFDAXRKLFWIISY 44

RESULT 11
US-08-475-845-2

```

SEQUENCE 2, Application US/08475845
Patent No. 5878895
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
    ADDRESS: Townsend and Townsend Khourie and Crew
    STREET: One Market Plaza, Steuart Street Tower
    CITY: San Francisco
    STATE: CA
    COUNTRY: U.S.A.
    ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PartnerLee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

RESULT 13
US-08-660-289-2
; Sequence 2, Application US/08660289
; Patent No. 5831982
; GENERAL INFORMATION:
; APPLICANT: Berkner, Kathleen L.
; APPLICANT: Petersen, Lars C.
; APPLICANT: Hart, Charles E.
; APPLICANT: Hedner, Ulla
; APPLICANT: Bregengaard, Claus
; TITLE OF INVENTION: Modified Factor VII
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24

```

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660,289
 FILING DATE: 08/06/2003
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/475,845
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/327,690
 FILING DATE: 28-FEB-1991
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parnelle, Steven W.
 REGISTRATION NUMBER: 31,910
 REFERENCE/DOCKET NUMBER: 13952-8-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-467-9600
 TELEX/FAX: 415-541-5043
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-660-289-2

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

RESULT 14
 US-08-537-807-2
 / Sequence 2, Application US/08537807
 / Patent No. 5861374
 / GENERAL INFORMATION:
 / APPLICANT: Modified Factor VII
 / TITLE OF INVENTION: Modified Factor VII
 / NUMBER OF SEQUENCES: 4
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.24
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/537,807
 / FILING DATE:
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Samisak, Deborah A.
 / REGISTRATION NUMBER: 31,438
 / REFERENCE/DOCKET NUMBER: 90-07C7
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 444 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 /

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05779
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: US 08/065,725
 FILING DATE: 21-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,920
 FILING DATE: 28-FEB-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Parnelle, Steven W.
 REGISTRATION NUMBER: 31,910
 REFERENCE/DOCKET NUMBER: 13952-8-1PC
 TELEPHONE: 206-467-9600
 TELEX/FAX: 415-541-5043

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-537-807-2

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

RESULT 15
 US-08-871-003-2
 / Sequence 2, Application US/08871003
 / Patent No. 5997864
 / GENERAL INFORMATION:
 / APPLICANT: Hart, Charles E.
 / APPLICANT: Petersen, Lars C.
 / APPLICANT: Hedner, Ulla
 / APPLICANT: Rasmussen, Mirella E.
 / TITLE OF INVENTION: Modified Factor VII
 / NUMBER OF SEQUENCES: 4
 / COMPUTER READABLE FORM:
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.24
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/871,003
 / FILING DATE:
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / CLASSIFICATION: 514
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Samisak, Deborah A.
 / REGISTRATION NUMBER: 31,438
 / REFERENCE/DOCKET NUMBER: 90-07C7
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 444 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 /

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Query Match Score 89.6%; Best Local Similarity 77.3%; Pred. No. 1.1e-20; Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Search completed: August 22, 2005, 09:37:01
 Job time : 44 sec

RESULT 3
 Sequence 3, Application US/10298330
 Publication No. US20030100506A1
 GENERAL INFORMATION:
 APPLICANT: Nelsetuen, Gary L.
 TITLE OF INVENTION: Modified Vitamin K-Dependent Polypeptides
 FILE REFERENCE: 09531-127001
 CURRENT FILING DATE: 2002-11-18
 PRIOR APPLICATION NUMBER: 09/419,591
 PRIOR FILING DATE: 2000-02-03
 PRIOR APPLICATION NUMBER: 09/302,239
 PRIOR FILING DATE: 1999-04-29
 PRIOR APPLICATION NUMBER: 08/935,636
 PRIOR FILING DATE: 1997-10-23
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 44
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: 6..7, 14..16, 19..20, 25..26, 29..35
 OTHER INFORMATION: Xaa = Gamma carboxyglutamic acid or glutamic acid
 US-10-298-330-3

Query Match 89.6%; Score 172; DB 14; Length 44;
 Best Local Similarity 100.0%; Pred. No. 5.7e-22;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ANAFLXXLRLPSSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44
 1 ANAFLXXLRLPSSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44

RESULT 3
 Sequence 3, Application US/1085506B
 Publication No. US20040220106A1
 GENERAL INFORMATION:
 APPLICANT: Nelsetuen, Gary L.
 TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT POLYPEPTIDES
 FILE REFERENCE: 09531-002001
 CURRENT APPLICATION NUMBER: US/10/855,068
 CURRENT FILING DATE: 2004-05-27
 PRIOR APPLICATION NUMBER: US/09/302,239
 PRIOR FILING DATE: 1999-04-29
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 44
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD RES
 LOCATION: (0)..(0)
 OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
 US-10-855-068-3

Query Match 89.6%; Score 172; DB 16; Length 44;
 Best Local Similarity 100.0%; Pred. No. 5.7e-22;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ANAFLXXLRLPSSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44
 1 ANAFLXXLRLPSSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44

RESULT 5
 US-09-782-587B-3
 Sequence 3, Application US/09782587B
 Publication No. US20030096333A1
 GENERAL INFORMATION:
 APPLICANT: PEDERSEN, ANDERS H.
 APPLICANT: BORNÆS, CLAUS
 APPLICANT: ANDERSON, KIM V.
 TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
 FILE REFERENCE: 31-001100US
 CURRENT FILING DATE: 2002-03-26
 PRIOR APPLICATION NUMBER: US/09/782,587B
 CURRENT FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: PA 2000 002218
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/184,036
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 19
 SEQ ID NO 1

Query Match 89.6%; Score 172; DB 10; Length 406;
 Best Local Similarity 100.0%; Pred. No. 5.3e-22;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44
 Db 1 ANAFLXXLRPGSLXRXCKXXQCSFXXARXIFKDAXRTKLFWIISY 44

RESULT 4
 US-09-782-587B-1
 Sequence 1, Application US/09782587B

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 406

TYPE: PRT

ORGANISM: Homo sapiens

US-09-782-587-B-3

RESULT 6

US-10-109-498-1

Sequence 1, Application US/10109498

Publication No. US20030044908A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

TITLE OF INVENTION: Coagulation Factor VII Derivatives

FILE REFERENCE: 6286_200-US

CURRENT APPLICATION NUMBER: US/10/109,498

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: PA 2001 00477

PRIOR FILING DATE: 2001-03-22

SEQ ID NO 1

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 406

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1) (406)

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-109-498-1

Query Match 89.6%; Score 172; DB 14; Length 406;

Best Local Similarity 100.0%; Pred. No. 5..3e-21;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1 ANAFLXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

1 ANAFLXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 8

US-10-281-727-1

Sequence 1, Application US/10281727

Publication No. US20030130191A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

APPLICANT: Olsen, Ole Hvilsted

APPLICANT: Human Coagulation Factor VII

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 6410_200-US

CURRENT APPLICATION NUMBER: US/10/281,727

PRIOR APPLICATION NUMBER: PA 2001 01627

PRIOR FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: 60/335,383

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 406

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: Xaa means 4-carboxyglutamic acid

OTHER INFORMATION: (gamma-carboxyglutamate)

US-10-281-727-1

Query Match 89.6%; Score 172; DB 14; Length 406;

Best Local Similarity 100.0%; Pred. No. 5..3e-21;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1 ANAFLXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

1 ANAFLXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 9

US-10-386-898-7

Sequence 7, Application US/10386898

Publication No. US20030229018A1

GENERAL INFORMATION:

APPLICANT: Kjalle, Marianne

APPLICANT: Jakobsen, Palle

APPLICANT: Hanning Ralf

TITLE OF INVENTION: DIMERIC TF ANTAGONIST

FILE REFERENCE: 6445_200-US

CURRENT APPLICATION NUMBER: US/10/386,898

PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373

PRIOR FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: US 60/365,935

PRIOR FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7

LENGTH: 406

TYPE: PRT

ORGANISM: human coagulation Factor VII

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (1) ..(406)

OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-386-898-7
 Query Match Score 172; DB 15; Length 406;
 Best Local Similarity 100.0%; Pred. No. 5.3e-21;
 Matches 44; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 SEQ ID NO 1 ANAFLXXLRPSSLXRXCXXQCSFXXARXIFKDAERTKLFWIISY 44
 Db 1 ANAFLXXLRPSSLXRXCXXQCSFXXARXIFKDAERTKLFWIISY 44

RESULT 10
 US-10-383-898-1
 ; Sequence 1, Application US/10381898
 ; Publication No. US2004009914A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Emory University
 ; TITLE OF INVENTION: Curcuminoid-protein conjugates
 ; FILE REFERENCE: E056 1060.1
 ; CURRENT APPLICATION NUMBER: US/10/383,898
 ; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CHAIN
 ; LOCATION: (1)..(406)
 ; US-10-383-898-1
 Query Match Score 172; DB 15; Length 406;
 Best Local Similarity 77.3%; Pred. No. 5.3e-21;
 Matches 34; Conservative 0; Mismatches 10;
 Indels 0; Gaps 0;
 SEQ ID NO 1 ANAFLXXLRPSSLXRXCXXQCSFXXARXIFKDAERTKLFWIISY 44
 Db 1 ANAFLEEERGSSLERKEEQCSFBEAREIFKDAERTKLFWIISY 44

RESULT 11
 US-10-617-500-1
 ; Sequence 1, Application US/10617500
 ; Publication No. US2004007255A1
 ; GENERAL INFORMATION:
 ; PRIOR APPLICATION NUMBER: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Stennicke, Henning R
 ; APPLICANT: Bjorn, Soren E
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: TF Antagonist
 ; FILE REFERENCE: 6510-200-US
 ; CURRENT APPLICATION NUMBER: US/10/617,500
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
 ; PRIOR FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1)..(406)
 ; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 ; US-10-617-500-1

Query Match Score 172; DB 15; Length 406;
 Best Local Similarity 100.0%; Pred. No. 5.3e-22;
 Matches 44; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 SEQ ID NO 2, Application US/10263205B
 ; Sequence 2, Application US/10263205B
 ; Publication No. US20040087498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKNER, Kathleen L.
 ; APPLICANT: PETERSEN, Lars
 ; APPLICANT: HART, Charles E.
 ; APPLICANT: HEDNER, Ulla
 ; APPLICANT: BREGENGAARD, Claus
 ; TITLE OF INVENTION: MODIFIED FACTOR VII
 ; FILE REFERENCE: 13952N-8-5-1
 ; CURRENT APPLICATION NUMBER: US/10/263,205B
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 08/464,029
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: 08/327,690
 ; PRIOR FILING DATE: 1994-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US94/05179
 ; PRIOR FILING DATE: 1994-05-23
 ; PRIOR APPLICATION NUMBER: 08/464,029
 ; PRIOR FILING DATE: 1993-05-21
 ; PRIOR APPLICATION NUMBER: PCT/US92/01636
 ; PRIOR FILING DATE: 1991-02-28
 ; PRIOR APPLICATION NUMBER: 07/662,920
 ; PRIOR FILING DATE: 1991-02-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-263-205B-2
 Query Match Score 172; DB 15; Length 406;
 Best Local Similarity 77.3%; Pred. No. 5.e-21;
 Matches 34; Conservative 0; Mismatches 10;
 Indels 0; Gaps 0;
 SEQ ID NO 3, Application US/10617619
 ; Sequence 1, Application US/10617619
 ; Publication No. US2004011092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bjorn, Soren E
 ; APPLICANT: Nicolaisen, Else M
 ; APPLICANT: Jorgensen, Anker S
 ; TITLE OF INVENTION: TF Binding Compound
 ; FILE REFERENCE: 6455-200-US
 ; CURRENT APPLICATION NUMBER: US/10/617,619
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: US 60/404,568
 ; PRIOR FILING DATE: 2002-08-19
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 406
 ; TYPE: PRT

```

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: MISC_FEATURE
; LOCATION: (1) ..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1

Query Match 89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44
Db 1 ANAFLXXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 14
US-10-701-294-1
; Sequence 1, Application US/10701294
; Publication No. US20040143092A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Back, Jakob M
; APPLICANT: Petersen, Lars C
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; FILE REFERENCE: 6608.200-US
; CURRENT APPLICATION NUMBER: US/10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
; PRIOR FILING DATE: 2002-12-20
; PRIOR FILING DATE: 2002-11-06
; SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1) ..(406)
; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-701-294-1

Query Match 89.6%; Score 172; DB 16; Length 406;
Best Local Similarity 100.0%; Pred. No. 5.3e-21;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44
Db 1 ANAFLXXLRPGSLXRCKXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 15
US-10-669-537-1
; Sequence 1, Application US/10669537
; Publication No. US20040192602A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; APPLICANT: Olsen, Ole Hvalsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544.200-US
; CURRENT APPLICATION NUMBER: US/10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 13
;
```

This Page Blank (uspto)

GenCore version 5.1.6	Aau77200	Human coa
Copyright (c) 1993 - 2005 Compugen Ltd.	Aau77192	Human coa
Protein - protein search, using sw model	Aau77190	Human coa
on: August 22, 2005, 09:28:04 ; search time 92 Seconds (without alignments)	Aau77198	Human coa
String table: BLOSUM62	Aau77193	Human coa
Score: US10031005-3G4	Aau77199	Human coa
Effect score: 198	Aau77201	Human coa
Influence: 1 ANAGFLXRLRGSSLRXCKX XXARXIFKDAXRTKLFWISY 45	Aau77188	Human coa
Gapext 0.5	Aau77194	Human coa
Gapopen 10.0 , Gapext 0.5	Aau77195	Human coa
Number of hits satisfying chosen parameters:	Aau77189	Human coa
Maximum DB seq length: 0	Aau77197	Human coa
Minimum DB seq length: 2000000000	Aab31688	Human coa
Number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Abb60178	Human Fac
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Abb60051	Human coa
SUMMARIES	Abb60069	Human coa
Result 1	Abb60072	Human coa
ID AAY18305 Standard; peptide: 44 AA.	Abb60071	Human coa
XX	Abb60068	Human coa
AC AAY18305;	Abb60070	Human coa
XX	Abb60070	Human coa
DT 17-AUG-1999 (first entry)	Abb60072	Human coa
XX	Abb60071	Human coa
DE Human factor VII GLA domain.	Abb60072	Human coa
XX	Abb60071	Human coa
KW GLA domain; vitamin K-dependent protein; clotting disorder; therapy.	Abb60072	Human coa
XX	Abb60071	Human coa
OS Homo sapiens.	Abb60072	Human coa
XX	Abb60071	Human coa
PN WO9920767-A1.	Abb60072	Human coa
XX	Abb60071	Human coa
PD 29-APR-1999.	Abb60072	Human coa
XX	Abb60071	Human coa
PP 20-OCT-1998;	Abb60072	Human coa
XX	Abb60071	Human coa
PR 23-OCT-1997;	Abb60072	Human coa
XX	Abb60071	Human coa
PA (MINU) UNIV MINNESOTA.	Abb60072	Human coa
XX	Abb60071	Human coa
PN Nelsestuen GL;	Abb60072	Human coa
XX	Abb60071	Human coa
DR WPI ; 1999-288309/24.	Abb60072	Human coa
XX	Abb60071	Human coa
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.	Abb60072	Human coa
XX	Abb60071	Human coa
Disclosure; Page 15; 86pp; English.	Abb60072	Human coa
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain.	Abb60072	Human coa
CC The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances CC membrane binding of the modified polypeptide as compared to the native CC polypeptide. The polypeptide is used to treat a clotting disorder by CC decreasing or increasing clot formation. Modification of the GLA domain CC results in a protein which has enhanced membrane binding affinity as CC compared to the native protein	Abb60072	Human coa
XX	Abb60071	Human coa
SQ Sequence 44 AA;	Abb60072	Human coa

Query Match	81.6%;	Score 161.5;	DB 2;	Length 44;	
Best Local Similarity	97.8%;	Pred. No. 6.1e-20;			
Matches	44;	Conservative	0;	Mismatches	1; Gaps 1;
Y	1 ANAGFLXXLRPGSLRXCXQQCSXXARXIFKDAKRTKLFWIYSY 45				
b	1 ANA-FLXXLRPGSLRXCXQQCSXXARXIFKDAKRTKLFWIYSY 44				
RESULT 2					
	AAB36395	standard; peptide; 44 AA.			
D	X				
X	C				
X	X				
T	T	(first entry)			
X	X	Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.			
X	X	Vitamin K-dependent protein; factor VII; protein C; GLA domain;			
X	X	Gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;			
X	X	Factor X; prothrombin; enhanced membrane binding affinity;			
X	X	clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;			
X	X	clotting disorder; haemophilia A; haemophilia B; liver disease.			
S	S	Homo sapiens.			
X	X				
X	N				
X	N				
D	D	WO200066753-A2.			
X	X	09-NOV-2000.			
X	X	28-APR-2000; 2000WO-US011416.			
X	X	29-APR-1999; 99US-00302239.			
X	X	(MINN) UNIV MINNESOTA.			
X	X	Nelsetuen GL;			
X	X	WPI; 2001-007226/01.			
X	X	Novel vitamin K-dependent polypeptide useful for treating clotting			
T	T	disorders such as thrombosis and hemophilia, comprises modified gamma-			
T	T	carboxy glutamic acid domain that enhances membrane binding affinity.			
S	S	Disclosure; Page 12; 81pp; English.			
C	C	The present invention describes a vitamin K-dependent polypeptide (I)			
C	C	comprising a modified gamma-carboxy glutamic acid (GLA) domain having at			
C	C	least one amino acid substitution, that enhances membrane binding			
C	C	affinity and the activity of the polypeptide relative to a corresponding			
C	C	native vitamin K-dependent polypeptide and inhibits clot formation. (I)			
C	C	can have thrombolytic and haemostatic activities, and can be used as an			
C	C	inhibitor of clot formation. (I) is useful for decreasing clot formation			
C	C	in a mammal, a factor VII or factor IX containing a modified GLA domain			
C	C	is useful for increasing clot formation and for treating a bleeding			
C	C	disorder, including thrombosis and clotting disorders such as haemophilia			
C	C	A, haemophilia B and liver disease. The present sequence represents a			
C	C	wild type human factor VII GLA domain sequence, given in the			
C	C	exemplification of the present invention			
X	X	Sequence 44 AA;			
Q	Q	RESULT 3			
Query Match	81.6%;	Score 161.5;	DB 4;	Length 44;	
Best Local Similarity	97.8%;	Pred. No. 6.1e-20;			
Matches	44;	Conservative	0;	Mismatches	1; Gaps 1;
Y	1 ANAGFLXXLRPGSLRXCXQQCSXXARXIFKDAKRTKLFWIYSY 45				
b	1 ANA-FLXXLRPGSLRXCXQQCSXXARXIFKDAKRTKLFWIYSY 44				

RESULT 3			
ID	ADD50096	standard;	protein; 44 AA.
ID	ADD50096	Human vitamin K-dependent protein #	
XX	XX		
XX	XX		
AC	AC	15-JAN-2004 (first entry)	
XX	XX		
DB	DB	Human; vitamin K-dependent protein;	
XX	XX	KW GLA domain; membrane binding affinity	
KW	KW	clotting disorder; site directed mutagenesis	
KW	KW	thrombolytic.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	US2003100506-A1.	
XX	XX		
PD	PD	29-MAY-2003.	
XX	XX		
PF	PF	18-NOV-2002; 2002US-00298330.	
XX	XX		
PR	PR	23-OCT-1997; 97US-00955636.	
XX	XX		
PR	PR	29-APR-1999; 99US-00302039.	
PR	PR	03-FEB-2000; 2000US-00497591.	
XX	XX		
PA	PA	(NELS/) NELSESTUEN G L.	
XX	XX		
PI	PI	Nelsetuun GL;	
XX	XX		
DR	WPI ; 2003-606646/57.		
XX	XX		
PT	PT	New vitamin K-dependent polypeptide	
PT	PT	mammals comprises a modified gamma-	
PT	PT	enhances membrane binding affinity	
XX	XX		
PS	Example 5; SEQ ID NO 3; 51pp; English		
XX	XX		
CC	The invention relates to a vitamin		
CC	K-dependent polypeptide comprising a modified gamma-carboxyglutamic acid		
CC	binding affinity and activity of the		
CC	corresponding native vitamin K-dependent		
CC	GLA domain comprises a glutamic acid		
CC	polypeptide is useful in modulating		
CC	treatment certain types of haemophilic		
CC	binding affinity of polypeptides is		
CC	mutagenesis in the GLA domain. This		
CC	dependent protein of the invention.		
XX	Sequence 44 AA;		
SQ			
Query Match	81.6%	Score	
Best Local Similarity	97.8%	Pred.	
Matches 44;	Conservative	0;	Mis
Qy	1 ANAGFLXXLRRPGSLXRXCXXXQCSPX		
Db	1 ANA-FIXXLRRPGSLXRXCXXXQCSPX		
RESULT 4			
ID	ADQ26902	standard;	protein; 44 AA.
ID	ADQ26902	Human factor VII gamma-carboxygluta-	
XX	XX		
AC	AC	cloy formation; protein C; a	
XX	XX		
DT	26-AUG-2004 (first entry)		
DB	DB		
KW	KW		

US6747003-B1.
008 - JUN - 2004.
003 - FEB - 2000; 2000US-00497591.
223 - OCT - 1997; 97US-00955636.
229 - APR - 1999; 99US-00302239.
(MINU) UNIV MINNESOTA.
Nelvestuen GL,
WPT; 2004-429803/40.

The invention relates to a method of decreasing clot formation comprising admixing to a patient an anticoagulant agent and a protein C or activated protein C (APC) polypeptide comprising a modified gamma-carboxyglutamic acid (GLA) domain with two, three, four or five amino acid substitutions. The invention also relates to vitamin K-dependent nucleic acids, polypeptides, host cells, vectors and antibodies used in the methods of the invention. The anticoagulant agent is aspirin, warfarin or heparin, preferably aspirin. The methods and compositions of the present invention are useful for modulating clot formation for treating haemophilic disorders in mammals. This sequence represents the human factor VII GLA domain, used in the method of the invention.

Sequence 44 AA;

Indels	Mismatches	Conservative	Similarity	Score	Length	Match
1	0	44	97.8%	81.3	61-203	1
1	0	44	97.8%	81.3	61-203	1
1	0	44	97.8%	81.3	61-203	1
1	0	44	97.8%	81.3	61-203	1

Γ_5
370 AAB84870 Standard; protein; 401 AA.
AAB84870:

Human; haemostatic; blood coagulant factor VII (FVII-31).
Human; haemophilic; blood coagulant factor VII; FVII; haemophilia;
murein.

PT	/note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp - Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"			
FT				
XX				
PN	JP2001061479-A.			
XX				
PD	13-MAR-2001.			
XX				
PF	99JP-00237610.			
XX				
PR	24-AUG-1999;			
XX	99JP-00237610.			
XX				
PA	(KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.			
XX				
DR	WPI; 2001-310677/33.			
XX				
N-FSDB	AAH19463.			
XX				
PT	Mutant of blood coagulant factor VII, used for substitution therapy in the treatment of haemophilia.			
XX				
PS	Claim 14; Page 20-21; 29PP; Japanese.			
XX				
CC	The present invention relates to mutants of blood coagulant factor VII (FVIIa). The present CC or activated blood coagulant factor VII (FVIIa). The present CC sequence is one such mutant FVII: VII-31. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients			
CC				
CC				
XX				
SQ	Sequence 401 AA;			
XX				
Query Match	81.6%	Score 161.5;	DB 4;	Length 401;
Best Local Similarity	75.6%	Pred. No. 5.9e-19;		
Matches	34;	Missmatches 10;	Indels 1;	Gaps 1
Conservative	0;			
Qy	1 ANAGFLXXLRPGSLRXCKXQCSPEXXARXIFKDAXRTLFKFWIY 45			
Db	1 ANA-FILEERPGSLRECKEFEQCSFEAREEIKFDAXRTLFKFWIY 44			
RESULT 6				
AAB84871	AAB84871 standard; protein; 401 AA.			
ID				
XX				
AC	AAB84871;			
XX				
DT	31-JUL-2001 (first entry)			
XX				
DB	Mutant blood coagulant factor VII (FVII-39) .			
XX				
XX	Human; haemostatic; blood coagulant factor VII; FVII; haemophilia; mutant; mutein.			
XX				
OS	Homo sapiens.			
XX				
OSynthetic.				
XX				
FH	Key Location/Qualifiers			
FT	Nisec-difference 235..239			
FT	/note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by Asp-Arg-Lys-Thr-Leu"			
FT	Nisec-difference 311..317			
FT	/note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp - Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"			
XX	JP2001061479-A.			
PN				
XX				
PD	13-MAR-2001.			
XX				
PF	99JP-00237610.			
XX				
PR	24-AUG-1999;			
XX	99JP-00237610.			
PA	(KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.			
XX				
DR	WPI; 2001-310677/33.			
XX				

PT Cleavage-site /note= "proteolytic site"
 PT /note= "proteolytic site"
 PT Disulfide-bond 44 .45
 PT Disulfide-bond 50 .61
 PT Disulfide-bond 55 .70
 PT Modified-site 63
 PT /label= OTHER
 PT /note= "beta-hydroxy-aspartic acid"
 PT Disulfide-bond 72 .81
 PT Disulfide-bond 91 .102
 PT Disulfide-bond 98 .112
 PT Disulfide-bond 114 .127
 PT Disulfide-bond 135 .162
 PT Cleavage-site 143 .144
 PT /note= "proteolytic site"
 PT Modified-site 145
 PT /note= "Glycosylation site"
 PT Disulfide-bond 159 .164
 PT Disulfide-bond 178 .194
 PT Active-site 193
 PT Active-site 242
 PT Cleavage-site 290 .291
 PT /note= "proteolytic site in unmodified factor VII"
 PT Misc-difference 290
 PT /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 PT Disulfide-bond 310 .329
 PT Cleavage-site 315 .316
 PT Modified-site 322
 PT /note= "proteolytic site"
 PT Disulfide-bond 340 .368
 PT Cleavage-site 341 .342
 PT /note= "glycosylation site"
 PT Active-site 344
 PT /note= "proteolytic site"
 PT Cleavage-site 392 .393
 PT /note= "proteolytic site"
 PT Cleavage-site 396 .397
 PT /note= "proteolytic site"
 PT Cleavage-site 402 .403
 PT /note= "proteolytic site"
 XX US5580560-A.
 PN XX
 PD 03 -DEC-1996.
 XX 22-AUG-1994; 94US-00293778.
 XX 13 -NOV-1989; 89US-00434149.
 PR 12 -JUN-1992; 92US-00888248.
 PR 09 -AUG-1993; 93US-00104509.
 XX (NOVO) NOVO-NORDISK AS.
 PA Wiberg FC, Woodbury R, Niccolaisen EM, Bjorn SE;
 XX DR; 1997-033523/03.
 XX Mutated human factor VII or VIIA proteins - with amino acid substitutions
 PT to improve proteolytic stability.
 XX Example 3 ; Page; 28pp; English.
 CC Modified human factor VII or VIIA proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32, Lys38,
 CC Ile42, Tyr44, Phe28, Arg104, Arg105, Tyr332 and Lys341 by an
 CC amino acid that provides a proteolytically more stable peptide bond.
 CC provided that Lys22 is replaced by Glu, His, Gly, Thr, Ala or Ser.
 CC The modified proteins are useful for treating bleeding disorders such as
 CC thrombocytopenia and von Willebrand's disease. They are also suitable for
 CC addition to plasma substitutes. The present sequence is a specific
 CC example of a modified Factor VII protein. (Updated on 25-MAR-2003 to
 CC correct PF field.)

XX SQ Sequence 406 AA;
 Query Match 81.6%; Score 161.5; DB 2; Length 406;
 Best Local Similarity 75.6%; Pred. No. 6e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCXXXQSFXKARXIFDAXRTKLFWIISY 45
 Db 1 ANA-FLEELRPGSLEREEBEKEQCSFEAREIFKDAERRKLFWIISY 44

RESULT 10
 AAU77745 AAU77745 standard; protein; 406 AA.
 ID AAU77745;
 XX
 AC AAU77745;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human factor VII active site mutant.
 XX Factor VII; human; shock heat treatment; protein stability;
 KW protein manufacture; protein conformation; mutant; mutant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Active-site 193
 /note= "Member of the factor VII catalytic triad"
 FT Active-site 242
 /note= "Member of the factor VII catalytic triad"
 FT Misc-difference 344
 /label= Gly, Met, Thr
 /note= "Preferably Ala. Wild type Ser"
 FT Active-site 344
 /note= "Member of the factor VII catalytic triad"
 XX WO200177141-A1.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-DK000234.
 PP
 XX 06-APR-2000; 2000DK-00000573.
 PR
 XX 17-APR-2000; 2000US-0197650P.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Matthiasen F;
 XX DR; 2001-657162/75.
 XX
 PT Stabilization of a polypeptide e.g. in a pharmaceutical composition
 PT involves a shock heat treatment.
 XX Disclosure; Page; 22pp; English.

PS
 XX
 CC The invention describes a method of stabilising a polypeptide involving
 CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition, in the industrial or large scale method of
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified human
 CC factor VII protein, mutated at the catalytic site, described in the
 CC invention. Note: This sequence does not appear in the specification but
 CC has been obtained using information given in the invention
 CC

PT Arg-Lys-Thr-Leu"
 XX JP2001061479-A.
 PN XX
 PD 13-MAR-2001.
 XX PP 24-AUG-1999; 99JP-00237610.
 XX PR 24-AUG-1999; 99JP-00237610.
 XX (KAGA) 2H KAGAKU & KESSEI RYOHKO KENKYUSHO.
 PA XX
 DR WPI; 2001-310677/33.
 DR N-PSDB; AAH19462.
 XX PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of haemophilia.
 XX PS Claim 9; Page 17-18; 29pp; Japanese.
 XX CC The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-30. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
 XX SQ Sequence 406 AA;
 PT Query Match 81.6%; Score 161.5; DB 4; Length 406;
 PT Best Local Similarity 75.6%; Pred. No. 6e-19;
 PT Matches 34; Conservative 0; Mismatches 10;
 PT Indels 1; Gaps 1;
 PT Qy 1 ANAGFLXXLRPGSLRXCXQCSFXAXRKFDAERTKLFWIYSY 45
 PT Db 1 ANA-FLEELRPGSLERECKEEQCSFEAREIFKDAERTKLFWIYSY 44
 XX
 RESULT 15
 ID AAM52183 standard; protein; 406 AA.
 XX AC AAM52183;
 XX XX
 PT DT 07-FEB-2002 (first entry)
 DE Human FVII mutant V253N.
 XX KW Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KW cardiac; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KW myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KW mutant.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key
 PT FT Misc-difference 6
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 7
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 14
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 16
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 19
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 20
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 25
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 26
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 29
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Misc-difference 35
 PT FT /label= Glu, OTHER
 PT FT /note= "OTHER = gamma carboxyglutamic acid"
 PT FT Modified-site 52
 PT FT /note= "O-glycosylated"
 PT FT Modified-site 60
 PT FT /note= "O-glycosylated"
 PT FT Modified-site 145
 PT FT /note= "N-glycosylated"
 PT FT Cleavage-site 152 . 153
 PT FT /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a
 PS Disclosure; Page 8-9; 29pp; Japanese.
 XX CC The present invention relates to mutants of blood coagulant factor VII (FVIIa). The present

FT Misc-difference 253 single disulphide bridge"
 FT /note= "Wild-type Val substituted by Asn"
 FT Modified-site 322
 FT /note= "N-glycosylated"
 XX WO200158935-A2.
 XX PD 16-AUG-2001.
 XX PP 12-FEB-2001; 2001WO-DK0000094.
 XX PR 11-FEB-2000; 2000DK-00000218.
 PR 18-OCT-2000; 2000DK-00001558.
 XX PA (MAXY-) MAXYGEN APS.
 XX PI Andersen KV, Pedersen AH, Bornaeus C;
 XX DR 2001-581807/65.
 XX PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as hemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently attached
 PT to polypeptide group.
 XX PS Example 3: Page: 89pp; English.
 XX CC The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC the polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the non-
 CC polypeptide group has been introduced or removed. The FVIIa conjugates
 CC have haemostatic, thrombolytic, cardiotonic, hepatotrophic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity. Note: The present sequence is not shown in the
 CC specification but is derived from the human wild-type FVII sequence shown
 CC in SEQ ID NO 1 (AAM52171)
 XX SQ Sequence 406 AA:

Query Match	81.6%	Score	161.5	DB	4	Length	406;		
Best Local Similarity	97.8%	Pred. No.	6e-19;	Mismatches	0;	Indels	1;	Gaps	1;
Matches	44;	Conservative	0;						

 Qy 1 ANAGFLXXLPGSLXIXCXXXQCSXXARXIFKDAXRTKDFWISY 45
 Db 1 ANA-FLXXLPGSLXIXCXXXQCSXXARXIFKDAXRTKDFWISY 44

This Page Blank (uspto)

A; Pathway: blood coagulation extrinsic pathway
 C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence #status predicted <SIG>
 F; 1-20/Domain: propeptide #status predicted <PRO>
 F; 1-104/Domain: Glu domain homology <GLA>
 F; 61-212/Product: coagulation factor VII light chain #status experimental <MA1>
 F; 1-141/Domain: EGF homology <EG1>
 F; 213-446/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F; 213-447/Domain: EGF homology <TRY>
 F; 66, 67, 74, 76, 79, 80, 85, 86, 89, 95/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
 F; 77-82, 110-121, 132-141, 151-162, 158-172, 174-187, 195-322, 219-224, 238-254, 370-389, 382/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 112-120/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 123/Modified Site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
 F; 212-213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F; 212-302/Active site: Arg-Tle (coagulation factor XIIa) #status predicted
 F; 350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match Score 161.5; Pred. No. 3.1e-19;
 Best Local Similarity 75.6%;保守性 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCXXQCSFXXARXIFKDAXRKLFWISY 45
 Db 61 ANA-FLEERPGSLRECKEIQCSFEEAREFKDAERTKLFWISY 104

RESULT 2
 I46332 coagulation factor VII - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C; Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C;Accession: I46932
 R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 R;Thromb. Res. 69, 231-238, 1993
 A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A;Reference number: I46332; PMID:8383365
 A;Accession: I46932
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-443 <BRO>
 A;Cross-references: GB:S56300; NID:9266294; PID:g266295
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 F; 2-83/Domain: Glu domain homology <GLA>
 F; 89-120/Domain: EGF homology <EG1>
 F; 130-166/Domain: EGF homology <EG2>
 F; 192-425/Domain: trypsin homology <TRY>

Query Match Score 127.5; DB 2; Length 443;
 Best Local Similarity 57.8%; Pred. No. 1.6e-13;
 Matches 26; Conserv性 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCXXQCSFXXARXIFKDAXRKLFWISY 45
 Db 40 ANA-FLEERPGSLRECKEIQCSFEEAREFKDAERTKLFWISY 83

RESULT 3
 KF07 coagulation factor VIIa (EC 3.4.21.21) - bovine
 C;Species: Bos primigenius taurus (cattle)
 C; Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C;Accession: A31979; C20274
 R;Takey, H.; Kawabata, S.; Nakagawa, K.; Yamamoto, Y.; Miyata, T.; Iwanaga, S.
 A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
 A;Reference number: A31979; PMID:89008362; PMID:304594
 A;Accession: A31979
 A;Molecule type: protein
 A;Residues: 1-407 <TAK>
 A;Cross-references: UNIPROT:P22457

R; McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor X
 A;Reference number: A20274; MUID:83308813; PMID:6688526
 A;Accession: C20274
 A;Molecule type: protein
 A;Residues: 58-62; X, 64-68 <MCM>
 A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, S.
 J. Biochem. 104, 867-868, 1988
 A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor X
 A;Reference number: A44556; MUID:89213999; PMID:3149637
 A;Contents: annotation
 A;Note: structure and location of covalently bound carbohydrate
 C;Function:
 A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A;Pathway: blood coagulation extrinsic pathway
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; coagulation factor VIIa light chain #status experimental <MA1>
 F; 1-44/Domain: Gla domain homology (Fragment) <GLA>
 F; 50-81/Domain: EGF homology <EG1>
 F; 51-127/Domain: EGF homology <EG2>
 F; 153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
 F; 153-387/Domain: trypsin homology <TRY>
 F; 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
 F; 17-22, 50-51, 55-70, 128-132, 159-164, 178-192, 262-267, 298-312, 340-368/I
 F; 53/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 145-203/Binding site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F; 15-153/Cleavage site: carbohydrate (Asn) (covalent) #status experimental
 F; 193-242,34/Active site: Arg-Tle (coagulation factor XIIa) #status experimental
 F; 290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted
 Query Match Score 119; DB 1; Length 407;
 Best Local Similarity 52.4%; Pred. No. 4.1e-12;
 Matches 22; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
 Qy 4 GFXXXLPGSLXRXCXXQCSFXXARXIFKDAERTKLFWISY 45
 Db 3 GFLELLPGSLRECREBLCSPEAHETFRNBERTRQFWVSY 44

RESULT 4
 JX0210 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N;Alternate names: vitamin K-dependent serine proteinase
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: JX0210
 A;Title: Isolation and characterization of a mouse protein C CDNA.
 A;Reference number: JX0210; MUID:92316897; PMID:1618739
 A;Accession: JX0210
 A;Molecule type: mRNA
 A;Residues: 1-461 <TD>
 A;Cross-references: UNIPROT:P31587; GB:D10445; NID:9220385; PMID:9220386
 A;Experimental source: liver
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that recognises beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence #status predicted <SIG>
 F; 1-33/Domain: Glu domain homology <GLA>
 F; 27-85/Domain: Glu domain homology <GLA>
 F; 34-41/Domain: protein C #status predicted <PRO>
 F; 42-196, 199-461/Domain: protein C #status predicted <PRC>
 F; 12-156/Domain: light chain #status predicted <PLC>
 F; 91-130/Domain: EGF homology <EG1>
 F; 139-174/Domain: EGF homology <EG2>
 F; 199-461/Domain: heavy chain #status predicted <PCH>
 F; 199-211/Domain: activation peptide #status predicted <ACT>

Query Match 49.7%; Score 98.5; DB 1; Length 461;
 Best Local Similarity 46.7%; Pred. No. 1.3e-08;
 Matches 21; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 09-Jul-2004
 C:Accession: A35827; PMID:222810

Qy 1 ANAGFLXXLRPGSLXRXCKXXQCSXXKARXKIFKDAXRTKLFWIISY 45
 Db 42 ANS-FLEEMPRPESLRECMEMICDFBAAQEIQFQNVEDTLAFWIKY 85

RESULT 5
 S10511 thrombin (EC 3.4.21.5) precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 09-Jul-2004
 C:Accession: S10511; A60576; B42696
 R:Dihanich, M.; Monard, D.
 Nucleic Acids Res. 18, 4551, 1990
 A:Title: cDNA sequence of rat prothrombin.
 A:Reference number: S10511; MUID:9032426; PMID:2377469
 A:Accession: S10511
 A:Molecule type: mRNA
 A:Residues: 1-617 <D1H>
 A:Cross-references: UNIPROT:P18292; EMBL:X52835; NID:956969; PIDN:CAA37017.1; PMID:956970
 R:Henriksson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
 Endocrinology 126, 167-175, 1990
 A:Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
 A:Reference number: A60576; MUID:90091942; PMID:1557383
 A:Accession: A60576
 A:Molecule type: protein
 A:Residues: 44-58 <HEN>
 A:Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uterus.
 R:Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing
 A:Reference number: A42696; MUID:92212913; PMID:1557383
 A:Status: preliminary

Query Match 49.7%; Score 98.5; DB 1; Length 461;
 Best Local Similarity 46.7%; Pred. No. 1.3e-08;
 Matches 21; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

C:Species: Mus musculus (house mouse)
 C:Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 09-Jul-2004
 C:Accession: A35827; PMID:222810

Qy 1 ANAGFLXXLRPGSLXRXCKXXQCSXXKARXKIFKDAXRTKLFWIISY 45
 Db 44 ANSGFLEELRKGNLERCVQCSVEEAFAEALSPQDTDVWAKY 88

RESULT 6
 A35827 thrombin (EC 3.4.21.5) precursor - mouse

R;Stenflo, J.; Fernlund, P.	R;Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.
J. Biol. Chem. 257, 12180-12190, 1982	Nature 299, 178-180, 1982
A;Title: Amino acid sequence of the heavy chain of bovine protein C.	A;Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A;Reference number: A18386; MUID:83007326; PMID:6896877	A;Reference number: I45891; MUID:8227386; PMID:6267289
A;Accession: A18386	A;Status: translated from GB/EMBL/DDJB
A;Molecule type: protein	A;Molecule type: mRNA
A;Residues: 157-454, 'PV'	A;Residues: 52-139 <CHO>
R;Bamon, N.L.; DeBault, L.E.; Bamon, C.T.	A;Cross-references: GB:J00007; NID:9163053; PID:AAA30520_1; PID:9163054
J. Biol. Chem. 258, 558-555, 1983	R;Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Suyoshi, T.; Miyata, T.
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F	J. Biochem. 104, 867-868, 1988
A;Reference number: A37541; MUID:8321513; PMID:6304092	A;Title: A new triosaccharide sugar chain linked to a serine residue in bovine blood coagulation factor Xa
A;Contents: annotation; activation; calcium binding	A;Reference number: A45556; MUID:89213999; PMID:319637
R;Johnson, A.B.; Bamon, N.L.; Lau, T.M.; Bamon, C.T.	A;Contents: annotation
J. Biol. Chem. 258, 555-556, 1983	A;Note: structure and location of a carbohydrate covalently bound to Ser
A;Title: Structural changes required for activation of protein C are induced by Ca ²⁺ -bind	C;Comment: Factor IX is activated by factor Xia, which excises the activation peptide pro-Xa.
A;Reference number: A37542; MUID:8321514; PMID:6406503	C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-dependent modification of the gamma-carboxyglutamic acid (Gla) residues and, with strong C;Function:
A;Contents: annotation; activation; calcium binding	C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; carboxyglutamic acid (Gla)
R;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re	C;Keywords: beta-hydroxyaspartic acid; calcium binding; calcium coagulation; calcium binding
s. C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a trypsin-like protease from the amino end of the heavy chain; this reaction C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong cognition of the thrombin-thrombomodulin complex.	F:1-146/Product: coagulation factor IXa light chain #status experimental
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin K-dependent modification of the gamma-carboxyglutamic acid (Gla) residues and, with strong C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology	F:1-45/Domain: Gla domain homology (Fragment) <GLA>
C;Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding	F:1-82/Domain: EGF homology <EG1>
F:1-29/Domain: signal sequence (fragment) #status predicted <SIG>	F:88-124/Domain: EGF homology <EG2>
F:21-83/Domain: Gla domain homology <GLA>	F:147-181/Domain: activation peptide #status experimental <AP1>
F:3-39/Domain: propeptide #status predicted <PRO>	F:182-116/Product: coagulation factor IXa heavy chain #status experimental <APC>
F:40-194/Product: protein C light chain #status experimental <LCH>	F:182-109/Domain: trypsin homology <TRY>
F:98-128/Domain: EGF homology <EG1>	F:7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F:177-172/Domain: EGF homology <EG2>	F:18-23, 51-52, 56-71, 73-82, 88-95-109, 111-124, 132-209, 207-223, 337-351, 362-390/Disulfide F:197-210/Domain: activation peptide #status experimental <AP1>
F:41-46, 53, 55, 58, 59, 62, 64, 65, 68, 74/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental	F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental	F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F:136, 289, 350/Binding site: carbohydrate (Asn) (covalent) #status predicted	F:158, 168, 173/6/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:232, 298, 397/Active site: His, Asp, Ser #status predicted	F:222, 270, 366/Active site: His, Asp, Ser #status predicted
F:366/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match 47.2%; Score 93.5; DB 1; Length 456;	Query Match 47.0%; Score 93; DB 1; Length 416;
Best Local Similarity 44.4%; Pred. No. 9.1e-08; Indels 1; Gaps 1;	Best Local Similarity 40.9%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 20; Conservative 5; Mismatches 19;	Matches 18; Conservative 7; Mismatches 19;
Db 40 ANS-PLEELRPQNYERECSEVCSEEEARIFQNTEDTMFAFWNSFY 83	Db 2 NSGKLEEVFVRGNLRECKECKSFEEAREVFENTERTEFWFKOY 45
RESULT 9	EXHU
	coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
	N;Alternate names: Stuart Factor
	C;Species: Homo sapiens (man)
	C;Accession: A24478; J00917; A220362; S39415; 154051; A005
	R;Levy, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
	R;Biochemistry 25, 509-5102, 1986
	A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e
	A;Reference number: A24478; MUID:87026600; PMID:3768336
	A;Molecule type: DNA
	A;Accession: A24478
	A;Residues: 1-488 <LEY>
	A;Cross-references: UNIPROT:P00742; GB:L29433; GB:M14327; GB:9459809; PID:9459809
	R;Messier, T.L.; Pittman, D.D.; Long, G.I.; Kaufman, R.J.; Church, W.R.
	Gene 99, 291-294, 1991
	A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor IXa (EC 3.4.21.22) precursor - bovine
	A;Reference number: J00917; MUID:91216473; PMID:1902434
KFB0	A;Accession: J00741
	A;Molecule type: mRNA
	A;Residues: 1-488 <MBE>
	A;Cross-references: GB:M57285; NID:9182399; PID:AAA52421_1; PID:9182390
	R;Miao, C.H.; Leyton, S.P.; Chung, D.W.; Davie, E.W.
	J. Biol. Chem. 267, 7395-7401, 1992
	A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
	A;Reference number: A42485; MUID:92218390; PMID:1313796
	A;Accession: A42485; MUID:92218390; PMID:1313796

A;Accession: A42485
A;Molecule type: DNA
A;Residues: 1-15 <MTA>
A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIP:93780, NCBIP:93787)
R;Kau, R.K.; Hildebrand, B.; Jagadeeswaran, P.
Gene 41, 311-314, 1986
A;Title: Isolation and characterization of human blood coagulation factor X cDNA.
A;Reference number: A25855 ; MUID:86221713; PMID:3011603
A;Accession: A2208
A;Molecule type: mRNA
A;Residues: 13-441,'S','443-488 <FIN>
A;Cross-references: GB:K03194; NID:9182840; PIDN:AA52490.1; PMID:g182841
R;Levytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Accession: A21284
A;Molecule type: mRNA
A;Residues: 13-284,'B',289-488 <LE2>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weintraub, KPHU
coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
N;Alternate names: antihemophilic factor B; Christmas factor
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
C;Accession: A00922; A7570; A30511; A32983; A22671; A37546; A30233; A60486; A20:
R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
Biochemistry 24, 3736-3750, 1985
A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
A;Reference number: A00922; MUID:86000558; PMID:2949176
A;Accession: A00922
A;Molecule type: DNA
A;Residues: 1-461 <YOS>
A;Cross-references: UNIPROT:P00740; GB:K02402; NID:9182612; PID:g182613
R;Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Broverman, EMBO J. 3, 1053-1060, 1984
A;Title: The gene structure of human anti-haemophilic factor IX.
A;Reference number: A37570; MUID:84235100; PMID:6329734
A;Accession: A37570
A;Molecule type: DNA
A;Residues: 1-461 <ANS>
A;Cross-references: GB:K02048
R;Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.J.K.; Riemens, A.; Briet, E.
Blood 72, 1074-1076, 1988
A;Title: The putative Factor IX gene promoter in hemophilia B Leyden.
A;Reference number: A30511; MUID:88327116; PMID:3416069
A;Accession: A30511
A;Molecule type: DNA
A;Residues: 8-24 <REI>
A;Cross-references: EMBL:X55508; NID:9311288; PIDN:CRB38245.2; PID:94469253
R;Koerber, D.D.; Bottema, C.D.K.; Buerstede, J.M.; Sommer, S.S.
A;Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulation factor IX.
A;Accession: A22673
A;Molecule type: mRNA
A;Residues: 1-193,'T',195-461 <MCG>

A;Accession: GDB:119890; OMIM:227600
A;Cross-references: GDB:119890
A;Map position: 13q14-13q34
A;Introns: 12-23 <RES>
A;Note: deletion of this factor causes Sturt disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the plasma
A;Pathway: blood coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
C;Comment: The two chains held together by one disulfide bond are formed from a single-chain polypeptide. The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
C;Genetics:
A;Gene: GDB:F10
A;Cross-references: 13q14-13q34
A;Map position: 24q1/; 77q3/; 86q1/; 124q1/; 150q3/; 249q3/; 289q1/1
A;Note: deletion of this factor causes Sturt disease
C;Function:
A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the plasma
A;Pathway: blood coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate
C;Comment: The two chains held together by one disulfide bond are formed from a single-chain polypeptide. The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or

- A;Cross-references: GB:M11309; PMID:9180552; PIDN:AA52023.1; PID:9180553
 A;Note: the authors translated the codon ACA for residue 29 as Tyr
 R;Jaye, M.; de la Salle, H.; Schamben, F.; Balland, A.; Kohli, V.; Findell, A.; Tolstoshe
 Nucleic Acids Res. 11, 2325-2335, 1983
 A;Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
 A;Reference number: A21337; MUID:63220786; PMID:6687940
 A;Accession: A21337
 A;Molecule type: mRNA
 A;Residues: 1-193, 'T', 195-461 <JAV>
 A;Cross-references: GB:J0013; PMID:9182610; PID:9182611
 R;Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A;Title: Isolation and characterization of a cDNA coding for human factor IX.
 A;Reference number: A30623; MUID:83065193; PMID:6959130
 A;Molecule type: mRNA
 A;Cross-references: GB:J00136; PMID:9182608; PIDN:AAA98726.1; PID:9182609
 A;Experimental source: liver
 R;Tharakarn, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A;Title: Development of an immunoaffinity process for factor IX purification.
 A;Reference number: A60866; MUID:90194857; PMID:2316207
 A;Molecule type: protein
 A;Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R;McMullen, B.A.; Fujikawa, K.; Kissiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IX.
 A;Reference number: A20274; MUID:83308813; PMID:6688526
 A;Accession: A20274
 A;Molecule type: protein
 A;Residues: 10-10, 'X', 111-115 <NCM>
 R;Balland, A.; Faure, T.; Carvalho, D.; Cerdier, P.; Ulrich, P.; Fournet, B.; de la Saill
 Eur. J. Biochem. 172, 565-572, 1988
 A;Title: Characterisation of two differentially processed forms of human recombinant Factor IX.
 A;Reference number: S0227; PMID:3280312
 A;Accession: S02527
 A;Molecule type: protein
 A;Residues: 28-63 <BAL>
 A;Note: processed forms expressed in recombinant system
 A;Accession: S12058; PMID:91006024; PMID:2209546
 A;Molecule type: mRNA; protein
 A;Residues: 1-68 <JAL>
 A;Note: processed forms expressed in recombinant system
 R;Handford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A;Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
 A;Reference number: S12377; MUID:90151623; PMID:2406129
 A;Molecule type: protein
 A;Residues: 92-130 <HAN>
 A;Note: NMR detection of calcium binding by domain expressed in recombinant system
 R;de la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A;Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A;Reference number: 159612; MUID:9405330; PMID:8236150
 A;Accession: S12377
 A;Molecule type: protein
 A;Status: translated from GB/EMBL/DDJB
 A;Residues: 444-461 <REES>
- A;Cross-references: GB:S66752; NID:9439773; PIDN:AAB28588.1; PID:9439774
 R;Ritofflet, E.S.; Koepfer, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A;Title: Genomic amplification with transcript sequencing.
 A;Reference number: 159529; MUID:88127096; PMID:3310835
 A;Accession: 159529
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 290-359 <RE2>
 A;Cross-references: GB:19063; PMID:AA52456.1; PID:9182623
 R;Agarwala, K.L.; Kawata, S.; Takao, T.; Murata, H.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A;Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
 A;Reference number: A54255; MUID:94227047; PMID:8172892
 A;Accession: A54255
 A;Molecule type: protein
 A;Residues: 'D', '204, 'X', 206-211; '212, 'D', '214, 'X', 215-221, 'D', <AGA>
 A;Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R;Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A;Title: Activation of human factor IX (Christmas factor).
 A;Reference number: A18483; PMID:78194509; PMID:655613
 A;Contents: annotation; activation; active site; carbohydrate binding
 R;McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984
 A;Contents: annotation
 A;Reference number: A37569
 A;Note: 194-Thr was also found
 R;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A;Title: Derivatives of blood coagulation factor IX contain a high affinity Ca²⁺-binding
 A;Contents: annotation; calcium binding
 R;Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A;Contents: annotation; calcium binding
 R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.C.
 Cell 45, 343-348, 1986
 A;Title: Defective propeptide processing of blood clotting factor IX caused by mutation <
 A;Reference number: A37545; PMID:8618994; PMID:3009023
 A;Contents: annotation; signal sequence; cleavage site
 R;Suehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A;Title: Blood clotting factor IX (BM) Nagoya: substitution of arginine 180 by tryptophan
 A;Reference number: A30622; PMID:90078229; PMID:2552373
 A;Contents: annotation; glycosylation, and cleavage sites
 A;Note: carboxylation; sequence of mutant B(M) Nagoya
 R;Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee
 submitted to the Brookhaven Protein Data Bank, November 1991
 A;Reference number: A51252; PDB:IIIXA
 A;Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A;Note: recombinant form expressed in yeast
 C;Comment: Factor IX is activated by factor Xia, which excises the activation peptide pro
 C;Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
 C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stro
 C;Genetics:
 A;Gene: GDB:F9
 A;Cross-references: GDB:119900; OMIM:306900
 A;Map position: Xq27.1-Xq27.2
 C;Pathway: blood coagulation intrinsic pathway
 C;Superfamily: coagulation factor X; EGFI homology; Glu domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PT>
 F:31-91/Domain: Glu domain homology <GLA>
 F:37-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGFI homology <EGI>
 F:134-170/Domain: EGFI homology <EG2>
 F:192-226/Domain: activation peptide #status experimental <ACT>

A;Residues: 1-461 <OKA>
 A;Cross-references: UNIPROT:P31394; EMBL:X64336; NID:956962; PIDN:CAA45617.1; PMID:956963
 R;Ogafuji, T.; Maekawa, K.; Nawa, K.; Maruyama, Y.
 Biochim. Biophys. Acta 1131, 329-332, 1992
 A;Title: The cDNA cloning and mRNA expression of rat protein C.
 A;Reference number: S24312; MUID:92329550; PMID:1627650
 A;Accession: S24312
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-461 <OKA2>
 A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PMID:956963
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
 F:1-32/Domain: signal sequence #status predicted <SIG>
 F:2-85/Domain: Gla domain homology <Gla>
 F:3-42/Domain: propeptide #status predicted <PRO>
 F:4-461/Product: protein C #status predicted <PRC>
 F:9-130/Domain: EGF homology <EG1>
 F:19-174/Domain: EGF homology <EG2>
 F:33-45/Domain: trypsin homology <TRY>
 F:47-48,55-57,60-61,66,67,70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F:112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:121-130,139-146-159,161-178,320-339-387,398-426/Disulfide bonds: #status
 F:25,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24,300,402/Active site: His, Asp, Ser #status predicted
 Query Match Score 89.5; DB 1; Length 461;
 Best Local Similarity 44.4%; Pred. No. 4.3e-07;
 Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;
 Db 42 ANS-PLEEVAGSLERECMEICDFEEAQIFQVNEDTLAFWKY 85

RESULT 13
 EXPR
 coagulation factor Xa (EC 3.4.21.6) precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C;Accession: S49075; JG9075; JC670; PS0190; 162745
 R;Stanton, C.; Ross, P.; Hudson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra
 A;Reference number: A5898; MUID:96093366; PMID:8570539
 A;Accession: S49075
 A;Molecule type: mRNA
 A;Residues: 1-482 <STA1>
 A;Cross-references: UNIPROT:Q63207; EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PMID:g5066
 A;Note: submitted to the EMBL Data Library, June 1994
 A;Note: neither the complete nucleic acid sequence nor the complete translation are show
 R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A;Reference number: JC670; MUID:96194815; PMID:8647460
 A;Accession: JC4670
 A;Molecule type: mRNA
 A;Residues: 1-482 <STA2>
 A;Experimental source: Cos-1 cell
 R;Eriyoshi, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 89-89, 1991
 A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
 A;Reference number: PS0190; MUID:92041742; PMID:1718949
 A;Accession: PS0191
 A;Molecule type: protein
 A;Residues: 41-58 'X' , 60-65 <ENJ1>
 A;Accession: PS0190
 A;Molecule type: protein
 A;Residues: 183-186 'X' , 188-207 <ENJ2>
 R;Murakawa, M.; Okamura, T.; Kuroiwa, T.; Kuroiwa, M.; Niho, Y.
 Eur. J. Haematol. 52, 162-165, 1994
 A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of

A;Reference number: 146196; MUID:94222160; PMID:8168596
 A;Accession: I6245
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA; PID:9455396
 A;Cross-references: GB:D21215; NID:9415309; PID:9455396
 C;Function:
 A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
 A;Pathway: blood coagulation
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <Gla>
 F:41-179/Product: coagulation factor X light chain #status predicted <LCX>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-482/Product: coagulation factor X heavy chain #status predicted <APT>
 F:184-231/Domain: activation peptide #status predicted <ACT>
 F:332-482/Domain: coagulation factor Xa heavy chain #status predicted <ACT>
 F:432-460/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,73/Modified site: gamma-carboxyglutamic acid (Glu) #statu
 F:77-62,90-110,95-110,112-121,129-149,151-164,172-341,238-243,539-575,388-402,41:
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:208/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:231-232/Cleavage site: Arg-Asp (Arg-Ile) (coagulation factor IXa, coagulation factor VIIa) #statu
 F:274,320,417/Active site: His, Asp, Ser #status predicted
 Query Match Score 85.5; DB 1; Length 482;
 Best Local Similarity 40.0%; Pred. No. 2.1e-06;
 Matches 18; Conservative 7; Mismatches 19; Indels 1; Gaps 1;
 Db 41 ANS-FEEBIIKGNLERECEVIECSPEAREVFEDNEETTEFWNKY 84

RESULT 14
 EXPR
 coagulation factor Xa (EC 3.4.21.22) precursor - dog
 A;Accession: A30351
 C;Species: Canis lupus familiaris (dog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A30351; I46201
 R;Evans, J.P.; Watzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1999
 A;Title: Molecular cloning of a cDNA encoding canine factor IX.
 A;Reference number: A30351; MUID:89323338; PMID:2752110
 A;Accession: A30351
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-452 <EVa>
 A;Cross-references: UNIPROT:P19540; GB:W21757; NID:9972719; PIDN:AAA30844.1; PMID:9163950
 R;Axelrod, J.H.; Read, M.S.; Brinkhous, K.M.; Verma, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A;Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic
 A;Reference number: A30351
 A;Accession: I46201
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-452 <AB>
 A;Cross-references: GB:M33826; NID:9163950
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-40/Domain: propeptide #status predicted <PRO>
 F:24-84/Domain: Gla domain homology <Gla>
 F:41-452/Product: coagulation factor IX #status predicted <NPT>
 F:90-121/Domain: EGF homology <EG1>
 F:127-163/Domain: EGF homology <EG2>
 F:218-45/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #st

F;57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di
F;258,306,402/Active site: His, Asp, Ser #status predicted

Query Match 42.9%; Score 85; DB 1; Length 452;
Best Local Similarity 38.6%; Pred. No. 2.4e-06;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 2 NAGFLXXLRPGSLXRXCKXXQCSFXKARXIFKDAKRTKLFWIISY 45
Db 41 NSGKLEEFVRGNLERECIEKCSFEEAREVFENTEKTEFKQY 84

RESULT 15

JQ0419 Coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JQ0419; I49667
R;Wu, S.M.; Stafford, D.W.; Ware, J.
Gene 86; 275-278, 1980
A;Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
A;Reference number: JQ0419; PMID:90215309; PMID:2323576
A;Accession: JQ0419
A;Molecule type: mRNA
A;Residues: 1-459 <WDS>
A;Cross-references: UNIPROT:P16294; GB:M23109; NID:9193317; PIDN:AAA37629_1; PID:g387158
A;Experimental source: liver
R;Sarkar, G.; Koebel, D.D.; Sommer, S.S.
Genomics 6;133-143, 1990
A;Title: Direct sequencing of the activation peptide and the catalytic domain of the fac
A;Reference number: I46580; PMID:90152675; PMID:2303254
A;Accession: I49667
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 168-362, 'Q' 364-387, 'I' 389-451 <RES>
A;Cross-references: GB:M26236; NID:9193319; PIDN:AAA37630_1; PID:g193320
C;Comment: This protein plays a critical role in blood coagulation.
C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-34/Domain: propeptide #status predicted <PRO>
F;19-79/Domain: Glu domain homology <GLA>
F;35-459/Domain: coagulation factor IX #status predicted <MAT>
F;85-116/Domain: EGF homology <EG1>
F;122-158/Domain: EGF homology <EG2>
F;225-452/Domain: trypsin homology <TRY>
F;41-42,49-51,54-55,60-61,64-67,70-74/Modified site: gamma-carboxyglutamic acid (Glu) #
F;52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/Di
F;265,313,409/Active site: His, Asp, Ser #status predicted

Query Match 42.9%; Score 85; DB 2; Length 459;
Best Local Similarity 38.6%; Pred. No. 2.5e-06;
Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 2 NAGFLXXLRPGSLXRXCKXXQCSFXKARXIFKDAKRTKLFWIISY 45
Db 36 NSGKLEEFVRGNLERECIEKCSFEEAREVFENTEKTEFKQY 79

Search completed: August 22, 2005, 18:46:44
Job time : 26 secs

This Page Blank (uspto)

Scoring table:	BLOSUM62	Alignments			
Gapopen:	10.0	Gapext:	0.5		
Searched:	1612378 seqs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378			
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
Database :	UniProt_03: 1: uniprot_sprot;* 2: uniprot_trembl;*				
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
		SUMMARIES			
Result No.	Score	Query	Match Length	DB ID	Description
--	--	--	--	--	--
1	161.5	FA7_HUMAN	466	1	P08709 homo sapien
2	161.5	FA7_HUMAN	81.6	2	Q96p68 homo sapien
3	127.5	FA7_RABBIT	61.6	2	P98129 orctolagus
4	119	FA7_BOVIN	64.4	1	P22457 bos taurus
5	118	FA7_MOUSE	59.6	1	Q8jhc9 brachydanio
6	116.5	FA7_PIG	58.8	1	P70375 mus musculus
7	103.5	FA7_XEN	52.3	1	Q9gkP2 sus scrofa
8	103	FA7_RAT	52.0	1	Q804x1 fugu rubripinnis
9	101	FA7_XEN	51.0	2	Q804x8 fugu rubripinnis
10	98.5	FA7_BOVIN	49.7	1	P33587 bos taurus
11	95	FA7_HUMAN	46.0	1	Q14668 homo sapien
12	95	FA7_RABBIT	48.0	1	Q8ne66 homo sapien
13	95	FA7_MOUSE	48.0	1	P18212 rattus norvegicus
14	95	FA7_PIG	48.0	1	P19221 mus musculus
15	93.5	FA7_RAT	47.2	1	Q8k3t6 rattus norvegicus
16	93	FA7_BOVIN	47.2	1	P00745 bos taurus
17	93	FA7_HUMAN	47.0	1	Q95mE8
18	93	FA7_BOVIN	47.0	1	Q95mE8
19	92.5	FA7_MOUSE	46.7	2	Q8PAG2
20	92	FA7_RABBIT	46.5	1	Q8TAS3
21	92	FA7_RAT	46.5	1	Q8TAS3
22	92	FA7_BOVIN	46.5	1	Q8TAS3
23	91.5	FA7_HUMAN	46.2	1	Q8TAS3
24	91	FA7_BOVIN	46.0	1	Q8TAS3
25	91	FA7_RABBIT	46.0	2	Q8TAS3
26	91	FA7_MOUSE	46.0	1	Q8TAS3
27	91	FA7_RAT	46.0	1	Q8TAS3
28	91	FA7_BOVIN	46.0	1	Q8TAS3
29	90.5	FA7_HUMAN	45.7	2	Q8TAS3
30	90.5	FA7_BOVIN	45.7	1	Q8TAS3
31	90	FA7_RABBIT	45.5	1	Q8TAS3
32			89.5	1	P31394 rattus norvegicus
33			89.5	2	Q68FV8 rattus norvegicus
34			89	2	Q6D1H4 xenopus tropicalis
35			88.5	2	Q804X5 gallus gallus
36			88	2	Q6SA95 felis silvestris catus
37			87.5	2	Q19045 orctolagus cuniculus
38			86	1	PA10_RABBIT
39			86	1	PA10_RABBIT
40			85.5	1	PA10_TROCA
41			85.5	2	PA10_TROCA
42			85	2	PA10_TROCA
43			85	1	PA9_CANEA canis familiaris
44			85	1	PA9_MOUSE mus musculus
45			84	1	PA10_HOPST hoplocephalus

- RL J. Biol. Chem. 266:11051-11057(1991).
- RN [6] STRUCTURE OF CARBOHYDRATE ON SER-112.
- RP MEDLINE=20062160; PubMed=2511201;
- RA Nishimura H., Kawabata S., Kisei W., Hase S., Ikenaka T., Takao T.,
- RA Shimonishi Y., Iwanga S.;
- RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl12-Glc-O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";
- RT Adv. Exp. Med. Biol. 264:2032-2035(1989).
- RN [7]
- RP STRUCTURE OF CARBOHYDRATE ON SER-112.
- RX MEDLINE=11344709; PubMed=212367;
- RA Iwanga S., Nishimura H., Kawabata S., Kisei W., Hase S., Ikenaka T.;
- RT "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z.";
- RT Adv. Exp. Med. Biol. 281:121-131(1990).
- RN [8]
- RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
- RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/38004a0;
- RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A., Konigsberg W.H., Nemreson Y., Kirchhofer D.;
- RA RT "The crystal structure of the complex of blood coagulation factor VIIa with soluble tissue factor.";
- RT Nature 380:41-46(1996).
- RN [9]
- RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
- RX MEDLINE=99126538; PubMed=9925787; DOI=10.1006/jmbi.1998.2452;
- RA Zhang B., St. Charles R., Tuinisky A.,
- RA RT "Structure of extracellular tissue factor complexed with factor VIIa inhibited with BPTI mutant.";
- RT RL J. Mol. Biol. 285:2089-2104(1999).
- RN [10]
- RP STRUCTURE BY NMR OF 105-145.
- RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
- RA Muranyi A., Finn B.E., Gippert G.P., Forssen S., Stenflo J., Drakenberg T.;
- RT "Solution structure of the N-terminal EGF-like domain from human factor VII.";
- RT RL Biochemistry 37:10605-10615(1998).
- RN [11]
- RP VARIANT GLN-364.
- RX MEDLINE=21300046; PubMed=2070047;
- RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J., Meade T.W., Tuddenham E.G.D.;
- RA RT "Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected male.";
- RT RL Blood 78:132-140(1991).
- RN [12]
- RP VARIANT GLN-364 AND PHB-370.
- RX MEDLINE=22340074; PubMed=1634227;
- RA Marchetti G., Ferrati M., Patracchini P., Gemmatti D., Derosa V., Pinotti M., Rodorigo G., Casonati A., Giroldi A., Bernardi F.;
- RA RT "Detection of two missense mutations and characterization of a repeat polymorphism in the factor VII gene (F7)." ;
- RT RL Hum. Genet. 89:497-502(1992).
- RN [13]
- RP VARIANT TYR-228.
- RX MEDLINE=33372811; PubMed=8364544;
- RA Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi F., von Feilitzsch A., Metz E., Hahn I., Prangnell D.R., Lumley H., Tuddenham E.G.D., McVey J.H., Aquilina A., Felice A.E.;
- RA RT "Two new missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of
- RT coagulation factor VII.";
- RL Hum. Mol. Genet. 2:1355-1359(1993).
- RN [15]
- RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
- RX MEDLINE=94264305; PubMed=8404879;
- RA Chaing S., Clarke B., Srihara S., Chu K., Friedman P., Vandusen W., Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
- RA RT "Severe factor VII deficiency caused by mutations abolishing the cleavage site for activation and altering binding to tissue factor.";
- RT RL Blood 83:3524-3535(1994).
- RN [16]
- RP VARIANT SER-367.
- RX PubMed=8860081;
- RA Devald G., Noethen M.M., Rutherford K., Redaelli R., Pinotti M., Lunghi B., Bernardi F., Casarman G., Redaelli R.,
- RT "A common Ser/Thr polymorphism in the perforin-homologous region of human complement component C7.";
- RT RL Hum. Hered. 44:301-304(1994).
- RN [17]
- RP VARIANT VAL-354.
- RX MEDLINE=95072589; PubMed=7981691;
- RA Rodeghiero F., Marchetti G., Bernardi F., Casarman G., Redaelli R.,
- RA RT "Topologically equivalent mutations causing dysfunctional coagulation factors VII (294Ala-->Val) and X (314Ser-->Pro)." ;
- RT RL Hum. Mol. Genet. 3:1175-1177(1994).
- RN [18]
- RP VARIANT MIE HIS-307.
- RX MEDLINE=95054662; PubMed=9743436;
- RA Ohwada M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
- RA RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by an amino acid substitution of His (CAC) for Arg (247) (CCG) in the catalytic domain.";
- RT RL Thromb. Haemost. 71:73-77(1994).
- RN [19]
- RP VARIANT MET-419.
- RX MEDLINE=96247510; PubMed=8652821;
- RA Arbini A.A., Mannucci P.M., Bauer K.A.;
- RA RT "Factor VII Mie: homozygous asymptomatic type I deficiency caused by an amino acid substitution of His (CAC) for Arg (247) (CCG) in the catalytic domain.";
- RT RL Thromb. Haemost. 71:73-77(1994).
- RN [20]
- RP VARIANT TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
- RX MEDLINE=97001216; PubMed=6644208;
- RA Arbini A.A., Mannucci P.M., Bauer K.A.;
- RA RT "A Thr>59Met mutation in Factor VII of a patient with a hereditary deficiency causes defective secretion of the molecule.";
- RT RL Blood 87:5055-5059(1996).
- RN [21]
- RP VARIANT VAL-304.
- RX MEDLINE=97037613; PubMed=8803260;
- RA Tamary H., Fromovich Y., Shammon L., Reich Z., Dym O., Lanir N., Brenner B., Paz M., Luder A.S., Blau O., Korotitshevsky M., Zaizov R., Seligsohn U.;
- RA RT "Factor VII Morioka (FVII L-26P): a homozygous missense mutation causing factor VII deficiency in Moroccan and Iranian Jews.";
- RT RL Thromb. Haemost. 76:283-291(1996).
- RN [22]
- RP VARIANT MORIOKA PRO-13.
- RX MEDLINE=98235713; PubMed=9576180;
- RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S., Sakuragawa N.;
- RA RT "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with Factor VII deficiency.";
- RT RL Br. J. Haematol. 101:47-49(1998).
- RN [23]
- RP VARIANT MALTA THR-194 AND VAL-304.
- RX MEDLINE=98112461; PubMed=9420302;
- RA Alshihawi C., Scerri C., Caldies R., Aquilina A., Felice A.E.;
- RA RT "Detection of missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of

RL	Hum. Mutat. Suppl. 1:S189-S191(1998).	Query Match [24]; Score 161.5; DB 1; Length 466;	81.6%;保守	Score 161.5; DB 2; Length 679;
RN	Best Local Similarity 75.6%; Pred. No. 1.6e-19; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	Best Local Similarity 75.6%; Pred. No. 2.3e-19; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;		
Qy	1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXFKDAXRTKLFWISY 45	Qy 1 ANAGFLXXLRPGSLRXCKXXQCSFXXARXFKDAXRTKLFWISY 45		
Db	61 ANA-FLEELRPGSLERECKEECSFEEARETFKDAERTKLFWISY 104	Db 39 ANA-FLEELRPGSLERECKEECSFEEARETFKDAERTKLFWISY 82		
RESULT 3				
	FA7_RABBIT	PRT; 444 AA.		
ID	FA7_RABBIT	STANDARD;		
AC	P98139; P79224; Created)	PRT;		
DT	01-DEC-2001 (T-EMBLref. 19, Created)	DT 01-PDB-1996 (Rel. 33, Created)		
DT	01-JUN-2003 (T-EMBLref. 24, Last sequence update)	DT 15-JUL-1998 (Rel. 36, Last sequence update)		
DT	01-MAR-2004 (T-EMBLref. 26, Last annotation update)	DT 25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Factor VII active site mutant immunoconjugate.	DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).		
DE	Homo sapiens (Human).	GN Name=F7;		
OS	Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Buteleostomi; Oryctolagidae; Lagomorpha; Leporidae; Oryctolagidae.	OS Oryctolagus cuniculus (Rabbit); Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Oryctolagidae; Lagomorpha; Leporidae; Oryctolagidae.		
OC	NCBI_TaxID:99606;	OC NCBI_TaxID:9966;		
OX	[1]	OX [1]		
RN	SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.		
RP	RC TISSUE=Liver;	RP REVISION TO 395.		
RX	RA MEDLINE=91190306; PubMed=8383365; DOI=10.1016/0049-3848(93)90048-S;	RX RA Brothers A.B.; Clarke B.J.; Blajchman M.A.; "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";		
RA	RJ Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).	RJ RT Thromb. Res. Suppl. 69:231-238(1993).		
RN	[2]	RN RN		
RP	SEQUENCE FROM N.A.	RP RP		
RA	RJ Z., Garen A.; "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostate cancer.";	RA Ruiz S.R.; Blajchman M.A.; Clarke B.J.; "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostate cancer.";		
RJ	RJ Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).	RJ RA Brothers A.B.; Clarke B.J.; Blajchman M.A.; "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";		
RN	[2]	RN RN		
RP	SEQUENCE FROM N.A.	RP RP		
RA	RJ Submitter (FEB-2003) to the EMBL/GenBank/DBJ databases.	RA Ruiz S.R.; Blajchman M.A.; Clarke B.J.; Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AP272274; AAC88686.2; -	RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.		
DR	HSSP; P08709; IKL1.	DR -		
DR	GO; GO:0005576; C:extracellular; IFA.	DR -		
DR	GO; GO:0005509; F:calcium ion binding; IFA.	DR -		
DR	GO; GO:0004295; F:peptidase activity; IFA.	DR -		
DR	GO; GO:0004295; F:trypsin activity; IFA.	DR -		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IFA.	DR -		
DR	IPR000152; ABX_hydroxy_1_S.	DR -		
DR	IPR000152; ABX_hydroxy_1_S.	DR -		
DR	IPR000742; EGF 2.	DR -		
DR	InterPro; IPR001881; EGF_Ca.	DR -		
DR	InterPro; IPR006209; EGF_Like.	DR -		
DR	InterPro; IPR007110; Ig_Like.	DR -		
DR	InterPro; IPR003597; Ig_Cl.	DR -		
DR	InterPro; IPR003066; Ig_NHC.	DR -		
DR	IPR001254; Peptidase S1.	DR -		
DR	IPR009003; Pept_Ser_Cys.	DR -		
DR	IPR000294; VitK_dep_GLA.	DR -		
DR	Pfam; PF07654; Cl-set; 2.	DR -		
DR	Pfam; PF00008; EGF; 1.	DR -		
DR	Pfam; PF00594; Gla; 1.	DR -		
DR	Pfam; PF00089; Trypsin; 1.	DR -		
SMART	SM00179; EGF_Ca; 1.	SMART; SM00069; GLA; 1.		
SMART	SM000407; IgCl; 1.	SMART; SM000407; IgCl; 1.		
SMART	SM00020; Trp_SPC; 1.	SMART; SM00020; Trp_SPC; 1.		
PROSITE	PS00010; ASX_HYDROXYL; UNKNOWN_1.	PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.		
PROSITE	PS00022; EGF; 1; UNKNOWN_1.	PROSITE; PS00022; EGF; 1; UNKNOWN_1.		
PROSITE	PS01186; EGF; 2; 1.	PROSITE; PS01186; EGF; 2; 1.		
PROSITE	PS50026; EGF; 3; 1.	PROSITE; PS50026; EGF; 3; 1.		
PROSITE	PS01187; EGF_Ca; 1.	PROSITE; PS01187; EGF_Ca; 1.		
PROSITE	PS00011; GLA; 1; 1.	PROSITE; PS00011; GLA; 1; 1.		
PROSITE	PS500290; TMPSIN_DOM; 1.	PROSITE; PS500290; TMPSIN_DOM; 1.		
PROSITE	PS500835; IG_LIKE; 2.	PROSITE; PS500835; IG_LIKE; 2.		
PROSITE	PS00240; TMPSIN_HIS; UNKNOWN_1.	PROSITE; PS00240; TMPSIN_HIS; UNKNOWN_1.		
PROSITE	PS00115; TMPSIN_SER; 1.	PROSITE; PS00115; TMPSIN_SER; 1.		
KW	EGF-Like domain; Hydrolase; Protease; Serine protease.	KW EGF Ca. domain; Hydrolase; Protease; Serine protease.		
SEQUENCE	679 AA; 75552 Mw; 0B023AA70A06/A1 CRC64;	SEQUENCE 679 AA; 75552 Mw; 0B023AA70A06/A1 CRC64;		

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sb-sib.ch).

EMBL; U77477; AAB37326.1; -.

HSSP; P0709; IFAK.

MEROPS; S01_215; -.

InterPro; IPR00151; Abx_hydroxy_1_S.

InterPro; IPR00742; EGF 2.

InterPro; IPR01881; EGF Ca.

InterPro; IPR01436; EGF II.

RESULT 5									
DR InterPro; IPR001314; Peptidase S1A.	Q8UHC9	PRELIMINARY;	PRT;	443	AA.				
DR InterPro; IPR000303; Pept_Ser_Cys.	Q8UHC9								
DR InterPro; IPR00294; VitK_dep_GLA.	AC								
DR Pfam; PF00008; EGF; 2.	Q8UHC9;								
DR Pfam; PF00594; Gla; 1.	AC	01-OCT-2002 (TREMBUREL 22, Created)							
DR Pfam; PF00089; Trypsin; 1.	DT	01-OCT-2002 (TREMBUREL 22, Last sequence update)							
DR PRINTS; PRO0722; CHYNOTRIPSIN.	DT	05-JUL-2004 (TREMBUREL 27, Last annotation update)							
DR PRINTS; PRO0010; EGFPLOOD.	DB	Coagulation factor VIII.							
DR PRINTS; PRO0001; GLABLOOD.	GN	Name=Ef71;							
DR SMART; SM00179; EGF_CA; 1.	OS	Brachydanio rerio (zebrafish) (Danio rerio).							
DR SMART; SM00069; Gla; 1.	RA	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
DR SMART; SM00020; TRYPC_SPC; 1.	OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;							
DR PROSITE; PS00010; ASX HYDROXYL; 1.	OC	Cyprinidae; Danio.							
DR PROSITE; PS00022; EGF; 1.	OX	CYPB1_TaxID=7935;							
DR PROSITE; PS01184; EGF; 2.	RN	[1] _							
DR PROSITE; PS00026; EGF; 3;	RP	SEQUENCE FROM N.A.							
DR PROSITE; PS01187; EGF_CA; 1.	RA	Hanumanthaiah R.; Day K.; Jagadeeswaran P.							
DR PROSITE; PS00011; Gla_-1;	RT	"Comprehensive analysis of blood coagulation pathways in Teleostei:							
DR PROSITE; PS00013; TRYPSIN HIS; 1.	CC	CC -I SIMILARITY: Belongs to peptidase family S1.							
DR PROSITE; PS00240; TRYPSIN DOM; 1.	CC	CC -I SIMILARITY: Contains 1 EGF-like domain.							
DR PROSITE; PS00155; TRYPSIN SER; 1.	DR	DR Evolution of coagulation factor genes and identification of zebrafish							
DR PROSITE; PS00014; BLOOD coagulation; Direct protein sequencing;	RT	factor VIII".							
KW BGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase.	RL	RL Blood Cells Mol. Dis. 0:0-0(2002).							
KW Repeat; Serine proteases; Vitamin K; Zymogen.	CC	CC -I SIMILARITY: Belongs to peptidase family S1.							
FT CHAIN 1 152 Factor VII light chain.	CC	CC -I SIMILARITY: Contains 1 EGF-like domain.							
FT CHAIN 153 407 Factor VII heavy chain.	DR	DR HSSP; P00740; 1CPH							
FT DOMAIN 1 45 Gla.	DR	DR ZFIN; ZDB-GENE-021206-10; f71.							
FT DOMAIN 46 82 EGF-like 1, calcium-binding (Potential).	DR	DR GO; GO:0005577; C:extracellular; IEA.							
FT DOMAIN 87 128 EGF-like 2.	DR	DR GO; GO:0005509; F:calcium ion binding; IEA.							
FT DOMAIN 153 407 Serine protease.	DR	DR GO; GO:0004263; F:chymotrypsin activity; IEA.							
FT SITE 152 153 Cleavage (by factor Xa, factor XIIa, factor IXa, or thrombin).	DR	DR GO; GO:0008233; F:peptidase activity; IEA.							
FT ACT SITE 193 193 By similarity.	DR	DR GO; GO:0004295; F:trypsin activity; IEA.							
FT ACT SITE 242 242 By similarity.	DR	DR GO; GO:0006505; F:proteolysis and peptidolysis; IEA.							
FT ACT SITE 344 344 By similarity.	DR	DR InterPro; IPR00742; EGF 2.							
FT BINDING 338 338 Substrate (By similarity).	DR	DR InterPro; IPR006209; EGF-like.							
FT DISULFID 17 22 By similarity.	DR	DR InterPro; IPR00383; GLA-blood.							
FT DISULFID 50 61 By similarity.	DR	DR InterPro; IPR006210; IEGF.							
FT DISULFID 55 70 By similarity.	DR	DR InterPro; IPR001254; Peptidase S1.							
FT DISULFID 72 81 By similarity.	DR	DR InterPro; IPR001314; Peptidase SIA.							
FT DISULFID 91 102 By similarity.	DR	DR InterPro; IPR009003; Pept_Ser_Cys.							
FT DISULFID 98 112 By similarity.	DR	DR InterPro; IPR00294; VitK_dep_GLA.							
FT DISULFID 114 127 By similarity.	DR	DR Pfam; PF00009; BGP; 1.							
FT DISULFID 135 262 By similarity.	DR	DR Pfam; PF00089; Trypsin; 1.							
FT DISULFID 159 164 By similarity.	DR	DR PRINTS; PR00722; CHYMOTRYPSIN.							
FT DISULFID 178 194 By similarity.	DR	DR SMART; SM00181; EGF; 2.							
FT DISULFID 310 329 By similarity.	DR	DR SMART; SM00089; GLA; 1.							
FT DISULFID 340 368 By similarity.	DR	DR SMART; SM00020; TRYPSIN; 1.							
FT MOD_RES 6 . 4-carboxyglutamate.	DR	DR PROSITE; PS00022; EGF 1.							
FT MOD_RES 7 7 4-carboxyglutamate.	DR	DR PROSITE; PS01186; EGF-2.							
FT MOD_RES 14 14 4-carboxyglutamate.	DR	DR PROSITE; PS50026; EGF; 1.							
FT MOD_RES 16 16 4-carboxyglutamate.	DR	DR PROSITE; PS00011; GLA; 1.							
FT MOD_RES 19 19 4-carboxyglutamate.	DR	DR PROSITE; PS50240; TRYPSIN; 1.							
FT MOD_RES 20 20 4-carboxyglutamate.	DR	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.							
FT MOD_RES 25 25 4-carboxyglutamate.	KW	KW EGF-like domain; Hydrolase; Protease; Serine protease.							
FT MOD_RES 26 26 4-carboxyglutamate.	SQ	SQ SEQUENCE 443 AA; 4823 MW; 2D2504718AE34FP4 CRC64;							
FT MOD_RES 29 29 4-carboxyglutamate.	Query Match	Query Match Score 118; DB 2; Length 443;							
FT MOD_RES 35 35 4-carboxyglutamate.	Best Local Similarity	Best Local Similarity 46.7%; Pred. No. 6, 8e-12;							
FT CARBOHYD 52 52 O-linked (Glc).	Matches 21;	Matches 8; Mismatches 16; Indels 0; Gaps 0; Gaps 0;							
FT CARBOHYD 145 145 N-linked (GlcNAc).	Db	Db 1 ANAGFLXXLRPGSLXRXCXXQCSFXAXIFKDAKRTKLFWIYS 45							
FT CARBOHYD 203 203 N-linked (GlcNAc).	Db	Db 38 ANSGFLEEMKAGNLRECRLCSFEAEHIFRNERTQFWVSY 44							
RESULT 6									
Qy 4 GFPXXXLRPGSLXRXCXXQCSFXAXIFKDAKRTKLFWIYS 45	FA7_MOUSE	ID FA7_MOUSE STANDARD;	PRT;	446	AA.				
Db 3 GFPLEELLPGLSLERECRELCSFEAEHIFRNERTQFWVSY 44	AC	P70375; 061109; STANDARD;							
	AC	01-NOV-1997 (Rel. 35, Created)							
	DT	01-NOV-1997 (Rel. 35, Last sequence update)							

RESULT	7
PRTC_PIG	
ID	PRTC_PIG
AC	Q9GLP2;
DT	16-OCT-2001
DT	16-OCT-2001

25-OCT-2004 (Rel. 45, Last annotation update)

DT Vitamin K-dependent protein C precursor (EC 3.4.21.69) (Anticoagulant protein C) (Blood coagulation factor XIV).

DE (Autoprothrombin II A) (Anticoagulant protein C) (Blood coagulation factor XIV).

DE Name=PROC;

GN Sub_scofra (Pig).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OC NCBI_TaxID=9823;

OX RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=21121490; PubMed=11229814;

RA Grimm D.R.; Colter M.B.; Braunschweig M.; Alexander L.J.; Neame P.J.; Kim H.K.W.;

RT "Porcine Factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains.";

RL Cell Mol. Life Sci. 58:148-159(2001).

CC -I- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIa in the presence of calcium ions and phospholipids.

CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.

CC -I- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.

CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

CC -I- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Gla domain. This Gla-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.

CC -I- SIMILARITY: Belongs to the peptidase S1 family.

CC -I- SIMILARITY: Contains 2 EGF-like domains.

CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

EMBL; AP11307; AA328380.1; -.

DR MEROPS; S01.21.8; -.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_Like.

DR InterPro; IPR02383; GLA_Blood.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR00903; Pept_Ser_Cys.

DR InterPro; IPR01254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR00291; Vitk_dep_GLA.

DR Pfam; PF00008; EGF_2.

DR Pfam; PF00594; Gla_1.

DR Pfam; PF00089; Trypsin_1.

DR PRINTS; PR00722; CHNOTRYSIN.

DR SMART; SM00001; GLABLOOD.

DR SMART; SM00669; GLA_1.

DR SMART; SM00020; TRYSPC_1.

DR PROSITE; PS00010; ASX_HYDROXYL_1.

DR PROSITE; PS00022; EGR_1.

DR PROSITE; PS00026; EGF_3.

DR PROSITE; PS01187; EGF_Ca_1.

DR PROSITE; PS00011; GLA_1.

DR PROSITE; PS00998; GLA_2.

DR PROSITE; PS00240; TRYPSIN_DOM.

DR PROSITE; PS00134; TRYPSIN_HIS.

DR PROSITE; PS00135; TRYPSIN_SER.

KW Blood coagulation; Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Hydroxylation; KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;

DR PROSITE; PS01186; EGF_2.

DR PROSITE; PS50026; EGF_3.

DR PROSITE; PS01187; EGF_Ca_1.

DR PROSITE; PS00011; GLA_1.

DR PROSITE; PS50098; GLA_2.

DR PROSITE; PS50240; TRYPSIN_DOM.

DR PROSITE; PS00134; TRYPSIN_HIS.

DR PROSITE; PS00135; TRYPSIN_SER.

KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;

FT SIGNAL 1 18

FT Repeat; Serine protease; Signal; Vitamin K.

FT SIGNAL 1 18

FT Repeat; Serine protease; Signal; Vitamin K.

FT PROPEP 19 41

FT CHAIN 42 459

FT CHAIN 42 196

FT PEPTIDE 199 213

FT SITE 213 214

FT DOMAIN 42 87

FT DOMAIN 96 131

FT DOMAIN 135 175

FT DOMAIN 214 459

FT MOD_RES 47 47

FT MOD_RES 48 48

FT MOD_RES 55 55

FT MOD_RES 57 57

FT MOD_RES 60 60

FT MOD_RES 61 61

FT MOD_RES 66 66

FT MOD_RES 67 67

FT MOD_RES 70 70

FT MOD_RES 112 112

FT ACT_SITE 255 255

FT ACT_SITE 301 301

FT ACT_SITE 400 400

FT DISUFID 58 63

FT DISUFID 91 110

FT DISUFID 100 105

FT DISUFID 104 119

FT DISUFID 121 130

FT DISUFID 139 150

FT DISUFID 146 159

FT DISUFID 161 174

FT DISUFID 182 221

FT DISUFID 240 256

FT DISUFID 371 385

FT CARBOHYD 396 424

FT CARBOHYD 138 138

FT CARBOHYD 292 292

FT CARBOHYD 353 353

SQ SEQUENCE 459 AA; 8541AAC14CC16D09 CRC64;

Query Match 52.3% Score 103.5; DB 1; Length 459;

Best Local Similarity 48.9%; Pred. No. 2.5e-09;

Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCXQCSFXARXIFKDAKRTKLFWIWSY 45

Db 42 ANS-FLEELRPPSLERCKETCDFEAREIFQNTENTMAFWFSKY 85

RESULT 8

Q804X1 ID Q804X1 PRELIMINARY;

AC Q804X1 DT 01-JUN-2003 (TREMBLrel. 24, Created)

AC DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

AC DT 01-JUN-2004 (TREMBLrel. 24, Last annotation update)

AC DT Coagulation factor VIIb (EC 3.4.21.21)

AC DE Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)

OS OS Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleosteoi; Neoteleosteoi;
 Acanthomorphia; Acanthopterygii; Teleostei; Tetraodontiformes;
 Teradontoidae; Tetraodontidae; Takifugu.

[1] NCBI_TaxID=31033 ;

SEQUENCE FROM N.A.
 Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 Tuddenham E.G.D., McVey J.H.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to peptidase family S1.

CC -!- SIMILARITY: Belongs to peptidase family S1.

EMBL: AF65274; AAC033369.1; - .

HSSP; P0707; 1CPH.
 GO; GO:0005509; C:extracellular; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003802; F:coagulation factor VIIa activity; IEA.
 DR GO; GO:0008233; F:coagulation factor activity; IEA.
 DR GO; GO:004295; F:tryptain activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR00152; Asx_hydroxy_S.
 DR InterPro; IPR00144; EGF_2.
 DR InterPro; IPR001881; EGF_Qa.
 DR InterPro; IPR005709; EGF_Tlike.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR003134; Peptidase_S1A.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR00394; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; GLA; 1.
 DR Pfam; PF00059; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Hydrolase; Protease; Serine protease.
 SEQUENCE 537 AA; 60449 MW; ABD40ADFB7F23851 CRC64;

Query Match Score 101; DB 2; Length 537;
 Best Local Similarity 40.9%; Pred. No. 8.1e-09;
 Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Db 2 NAGFLXXLRPGSLXRXCXXQCSFXXXKXIFKDAXRTKLFWISY 45
 47 NSCHLEIQKDNLERECKEEOCTMEEAREVFDEKTAEFWVGY 90

RESULT 10

PTC_MOUSE STANDARD; PRT; 460 AA.
 ID PTC_MOUSE STANDARD; PRT;
 AC P33598; Q99PC6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DB Vitamin K-dependent Protein C precursor (BC 3.4.21.69)
 DE (Autoprothrombin IIa) (Anticoagulant protein C) (Blood coagulation factor XIV).
 DE Name=PROC;
 GN STRAIN-BALB/C; TISSUE-Liver;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 NCBI_TaxID=10090;

RN [1] Isolation and characterization of a mouse protein C cDNA.
 RN Sequence from N.A.
 RC STRAIN-BALB/C; TISSUE-Liver;
 RX MEDLINE=9231689; PubMed=1618739;

RN [2] Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RL J. Biochem. 111:491-495 (1992).

RN Sequence from N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

[1] NCBI_TaxID=31033 ;

RP Sequence from N.A.
 RA Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 RA Tuddenham E.G.D., McVey J.H.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

[1] NCBI_TaxID=31033 ;

RX MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen B.D., Lisbess A., Carmeliet P., Collen D.,
 Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 anticoagulant protein C."
 RL Thromb. Haemost. 79:310-316(1998).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6;
 RC Korf I.;
 RT "Complete sequence of UC72A01";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDJB databases.
 [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=22388257; PubMed=124771932; DOI=10.1073/pnas.242603399;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 Altsechler B., Schaefer C.F., Bhat N.K.,
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Whaley J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grinowicz J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]

RN SEQUENCE OF 274-433 FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=94318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
 RT "A comparative study of partial primary structures of the catalytic
 region of mammalian protein C";
 RL Br. J. Haematol. 86:590-600 (1994).

-1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 regulates blood coagulation by inactivating factors Va and VIIa
 in the presence of calcium ions and phospholipids.

-1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 and VIIa.

-1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 into a light chain and a heavy chain held together by a disulfide
 bond. The enzyme is then activated by thrombin, which cleaves a
 tetradecapeptide from the amino end of the heavy chain; this
 reaction, which occurs at the surface of endothelial cells, is
 strongly promoted by thrombomodulin.

-1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 residues allows the modified protein to bind calcium.

-1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 another site, beyond the GLA domain. This GLA-independent binding
 site is necessary for the recognition of the thrombin-
 thrombomodulin complex.

-1- SIMILARITY: Belongs to the peptidase S1 family.

-1- SIMILARITY: Contains 2 EGF-like domains.

-1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to licensee@isb-sib.ch).

CC CC

DR EMBL; D10445; BAA01235.1; -.
 DR EMBL; AF034569; AAC33795.1; -.
 DR EMBL; AF518182; AAC07918.1; -.
 DR EMBL; BC013895; AAH13896.1; -.
 DR EMBL; D43755; BAA07812.1; -.
 DR PIR; JX0210; JX0210.
 DR HSSP; P04070; IAUT.
 DR MEROPS; S01.21.8; -.
 DR MGD; MGI:19771; PROC.
 DR InterPro; IPR00155; Abx_hydroxyl_S.
 DR InterPro; IPR001742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006204; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR009003; Peptidase_S1.
 DR InterPro; IPR01254; Peptidase_S1A.
 DR InterPro; IPR01314; Peptidase_S1A.
 DR InterPro; IPR000294; VitK_dep_GLAs.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; Gla_1.
 DR Pfam; PF00089; Trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABL00D.
 SMART; SM00179; EGF_CA_1.
 SMART; SM00063; GLA_1.
 SMART; SM00020; TRYD_SPE_1.
 DR PROSITE; PS00010; ASX_HYDROXYL_1.
 DR PROSITE; PS00022; EGF_1.
 DR PROSITE; PS01186; EGF_2.
 DR PROSITE; PS50026; EGF_3.
 DR PROSITE; PS01187; EGF_CA_1.
 DR PROSITE; PS00011; GLA_1.
 DR PROSITE; PS50098; GLA_2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SRR; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Hydroxylation;
 KW Gamma-carboxyglutamic acid; Signal; Vitamin K.
 KW Repept; Serine protease; Signal; Vitamin K.
 FT SIGNAL; 1 33 By similarity.
 FT PROBP; 34 41 By similarity.
 FT CHAIN; 42 460 Vitamin K-dependent protein C.
 FT CHAIN; 42 196 Vitamin K-dependent protein C light chain
 (By similarity).
 FT CHAIN; 199 460 Vitamin K-dependent protein C heavy chain
 (By similarity).
 FT PEPTIDE; 199 212 Activation peptide (By similarity).
 FT SITE; 212 213 Cleavage (by thrombin) (By similarity).
 FT DOMAIN; 42 87 Gla_1.
 FT DOMAIN; 96 131 EGF-like 1.
 FT DOMAIN; 135 175 EGF-like 2.
 FT DOMAIN; 213 460 Serine protease.
 FT MOD_RES; 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES; 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES; 55 55 4-carboxyglutamate (By similarity).
 FT MOD_RES; 57 57 4-carboxyglutamate (By similarity).
 FT MOD_RES; 60 60 4-carboxyglutamate (By similarity).
 FT MOD_RES; 61 61 4-carboxyglutamate (By similarity).
 FT MOD_RES; 66 66 4-carboxyglutamate (By similarity).
 FT MOD_RES; 67 67 4-carboxyglutamate (By similarity).
 FT MOD_RES; 70 70 4-carboxyglutamate (By similarity).
 FT MOD_RES; 112 112 3-hydroxyaspartate (By similarity).
 FT ACT_SITE; 253 253 Charge relay system.
 FT ACT_SITE; 299 299 Charge relay system.
 FT ACT_SITE; 401 401 Charge relay system.
 FT DISUFDID; 58 63 By similarity.
 FT DISUFDID; 91 110 By similarity.
 FT DISUFDID; 100 105 By similarity.
 FT DISUFDID; 104 119 By similarity.
 FT DISUFDID; 121 130 By similarity.
 FT DISUFDID; 139 150 By similarity.

RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwade J.J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Smialius D.E., Schniech A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	SEQUENCE FROM N.A.
RC	TISSUE:Testis;
RA	Straubberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR	BC030786; AAH30786; -.
DR	HSSP; P00740; 1CFH.
DR	GO; GO:000576; C:extracellular; IEA.
DR	GO; GO:000509; F:calcium ion binding; IEA.
DR	InterPro; IPR002383; GLA_blood.
DR	InterPro; IPR000284; VitK_dep_GLA.
DR	Pfam; PF00594; Gla; 1.
DR	PRINTS; PRO0001; GLABLOOD.
DR	SMART; SM00069; GLA; 1.
DR	PROSITE; PS00001; GLA; 1..1.
FT	NON_TER 1
SQ	266 AA; 30151 MN; 175768D24D635351 CRC64;
Query Match	48.0% ; Score 95; DB 2; Length 266;
Best Local Similarity	40.5% ; Pred. No. 4.6e-08;
Matches	17; Conservative 8; Nismatches 17; Indels 0; Gaps 0;
Qy	4 GFLXXLRPGSLRXCKXXXQGSFXXARXIFKDAXRXTLFWISY 45
Db	71 GPFEEIRQNIERRECKEEFCTFEAREAFENNEKTEKFWMSTY 112
RESULT 13	
THR_B RAT	SEQUENCE FROM N.A.
ID	THR_B RAT
AC	P18292;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DB	Prothrombin precursor (EC 3.4.21.5).
GN	Name=F2; Name=R2;
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TAXID	10116;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague-Dawley; TISSUE=Liver;
RC	PubMed=9222913; PubMed=15557383;
RX	PubMed=90312426; PubMed=2377469;
RA	Dihanich M.; Monard D.;
RA	"cDNA sequence of rat prothrombin.";
RT	Nucleic Acids Res. 18:4251-4251 (1990).
RL	[2]
RN	SEQUENCE OF 383-617 FROM N.A.
RP	SEQUENCE OF 383-617 FROM N.A.
RC	TISSUE=liver;
RX	PubMed=9222913; PubMed=15557383;
RA	Banfield D., Magilivray R.T.;
RA	"Partial characterization of vertebrate prothrombin cDNAs:
RT	amplification and sequence analysis of the B chain of thrombin from nine different species.";
RT	Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).
RT	-1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombinodulin, protein C.
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B.
CC	-1- PTM: The gamma-carboxylglutamyl residues, which bind calcium ions, result from the carboxylation of glutamyl residues by a microsomal enzyme, the taurin K-dependent interaction with a
CC	are necessary for the calcium-dependent interaction with a modified residues

negatively charged phospholipid surface, which is essential for the conversion of prothrombin to thrombin.

- MISCELLANEOUS: Prothrombin is activated on the surface of a phospholipid membrane that binds the amino end of prothrombin and factors Va and Xa in Ca-dependent interactions; factor Xa removes the activation peptide and cleaves the remaining part into light and heavy chains. The activation process starts slowly because factor V itself has to be activated by the initial, small amounts of thrombin.

- MISCELLANEOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation by factor Xa.

- SIMILARITY: Belongs to the peptidase S1 family.
- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
- SIMILARITY: Contains 2 kringle domains.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR	E52855; QAA37017.1;	-.
CC DR	EMBL; M1397; AAA42240.1;	-.
CC DR	PIR; S10511; S10511.	.
CC DR	HSSP; P00734; IUVS.	.
CC DR	MEROPS; S01.2117; -.	.
CC DR	RGD; 61996; F2.	GLA blood.
CC DR	InterrPro; IPR002383;	GLA
CC DR	InterPro; IPR000101;	Kringle.
CC DR	InterPro; IPR009003;	Pept Ser Cys.
CC DR	InterPro; IPR001254;	PeptIdase_S1.
CC DR	InterPro; IPR001314;	PeptIdase_S1A.
CC DR	InterPro; IPR003966;	PeptIdase_S1A_pr.
CC DR	InterPro; IPR000294;	VitK_dep_GLAs.
CC DR	Pfam; PF00094;	Kringle.
CC DR	Pfam; PF00051;	Kringle.
CC DR	Pfam; PF00089;	Trypsin.
CC DR	PRINTS; PRO0022;	CHMTRYDPSIN.
CC DR	PRINTS; PRO00001;	GLABLOOD.
CC DR	PRINTS; PRO00018;	KRINGLE.
CC DR	PRINTS; PRO15005;	PROTHROMBIN.
CC DR	PRODOM; PD000035;	Kringle.
CC DR	SMART; SM00069;	GLA.
CC DR	SMART; SM00130;	KR.
CC DR	SMART; SM00020;	TRYP_SPC.
CC DR	PROSITE; PS000011;	GLA.
CC DR	PROSITE; PS50938;	GLA.
CC DR	PROSITE; PS00001;	KRINGLE.
CC DR	PROSITE; PS50070;	KRINGLE.
CC DR	PROSITE; PS50240;	TRYPSIN_DOM.
CC DR	PROSITE; PS00014;	TRYPSIN_HIS.
CC DR	PROSITE; PS00015;	TRYPSIN_SER.
KW Acute phase; Blood coagulation; Calcium-binding;		
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Kringle; Plasma;		
KW Repeat; Serine protease; Signal; Vitamin K; Zymogen.		
FT SIGNAL	1	24
FT PROPEP	25	43
FT CHAIN	44	617
FT PEPTIDE	44	200
FT PEPTIDE	201	323
FT CHAIN	324	359
FT CHAIN	360	617
FT DOMAIN	44	90
FT DOMAIN	109	187
FT DOMAIN	215	292
FT DOMAIN	360	617
FT SITE	200	201
FT SITE	323	324
FT SITE	359	360

Prothrombin.
Activation peptide (fragment 1).
Activation peptide (fragment 2).
Thrombin light chain.
Thrombin heavy chain.
Gla.
Kringle 1.
Kringle 2.
Serine protease.
Cleavage (by thrombin).
Cleavage (by factor Xa).
Cleavage (by factor Xa).
Cleavage (by factor Xa).

PRINTS; PRO0722; CHYMOTRYPSIN.	
DR PRINTS; PRO0001; GLABLOOD.	
DR PRINTS; PRO0018; KRINGLE.	
DR PRINTS; PRO0150; PROTHROMBIN.	
DR PRODom; PRO00395; Kringle; 2.	
DR PROSITE; PS00011; GLA; 1; 1.	
DR PROSITE; PS00998; GLA; 2; 1.	
DR PROSITE; PS00021; KRINGLE; 1; 2.	
DR PROSITE; PS00070; KRINGLE; 2; 2.	
DR PROSITE; PS0240; TRYPSIN_DOM; 1.	
DR PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR PROSITE; PS00125; TRYPSIN_SER; 1.	
KW Acute phase; Blood coagulation; Calcium-binding;	
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Plasma;	
KW Repeat; Serine protease; Signal; Vitamin K; Zymogen.	
FT SIGNAL 1 24	Potential.
PROPEP 25	
FT CHAIN 44 43	Prothrombin.
FT PEPTIDE 44 618	Activation peptide (fragment 1).
FT PEPTIDE 201 200	Activation peptide (fragment 2).
FT CHAIN 325 324	Cleavage (By thrombin).
FT CHAIN 360 325	Cleavage (By factor Xa).
FT DOMAIN 44 361	Cleavage (By light chain).
FT DOMAIN 44 618	Thrombin heavy chain.
FT DOMAIN 109 107	Gla.
FT DOMAIN 215 292	Kringle 1.
FT DOMAIN 361 292	Kringle 2.
FT SITE 200 201	Serine protease.
FT SITE 565 565	Cleavage (By thrombin).
FT SITE 565 565	Cleavage (By factor Xa).
FT ACT_SITE 403 403	Charge relay system (By similarity).
FT ACT_SITE 459 459	Charge relay system (By similarity).
FT MOD_RES 50 50	Charge relay system (By similarity).
FT MOD_RES 51 51	4-carboxyglutamate.
FT MOD_RES 58 58	4-carboxyglutamate.
FT MOD_RES 60 60	4-carboxyglutamate.
FT MOD_RES 63 63	4-carboxyglutamate.
FT MOD_RES 64 64	4-carboxyglutamate.
FT MOD_RES 69 69	4-carboxyglutamate.
FT MOD_RES 70 70	4-carboxyglutamate.
FT MOD_RES 73 73	4-carboxyglutamate.
FT MOD_RES 76 76	4-carboxyglutamate.
FT DISULFID 61 66	4-carboxyglutamate.
FT DISULFID 91 104	By similarity.
FT DISULFID 109 107	By similarity.
FT DISULFID 130 170	By similarity.
FT DISULFID 158 182	By similarity.
FT DISULFID 215 293	By similarity.
FT DISULFID 236 276	By similarity.
FT DISULFID 264 289	By similarity.
FT DISULFID 333 479	Interchain (By similarity).
FT DISULFID 388 404	By similarity.
FT DISULFID 533 547	By similarity.
FT DISULFID 561 591	By similarity.
FT CARBOHYD 122 122	N-linked (GlcNAc . .).
FT CARBOHYD 144 144	N-linked (GlcNAc . .).
FT CARBOHYD 413 413	N-linked (GlcNAc . .).
FT CARBOHYD 553 553	N-linked (GlcNAc . .).
SQ SEQUENCE 618 AA; 70268 MW; B89F719AED601B0 CRC64;	
Query Match 48.0%; Score 95; DB 1; Length 618;	
Best Local Similarity 42.2%; Pred. No. 1..1e-07;	
Matches 19; Conservative 5; Mismatches 21; Indels 0; Gaps	
Qy 1 ANAGFLXLRLPSSLXRCKXQOSFXXXRKFDAKRTKLWIVSY 45	
Db 44 ANSGFLEELRKGNLERCVEEQSYEEAFAELESPOQTDVFWAKY 88	
RESULT 15	
FA7_FAT ID FA7_FAT	
AC Q8K3U6	

PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_-; 1.
DR PROSITE; PS5098; GLA_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
Blood coagulation; Calcium-binding; EGF-like domain; Hydrolase; Hydroxylation;
KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.
SIGNAL 1 24 Potential.
FT PROPEP 25 41 Factor VII light chain (By similarity).
FT CHAIN 42 193 Factor VII heavy chain (By similarity).
FT DOMAIN 42 446 Gla.
FT DOMAIN 87 123 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 128 169 EGF-like 2.
FT DOMAIN 194 446 Serine protease.
FT SITE 193 194 Cleavage by factor Xa, factor XIIa,
factor IXa, or thrombin (By similarity).
FT ACT_SITE 234 234 By similarity.
FT ACT_SITE 283 283 By similarity.
FT ACT_SITE 385 385 By similarity.
FT BINDING 379 379 Substrate (By similarity).
FT DISULFID 58 63 By similarity.
FT DISULFID 91 102 By similarity.
FT DISULFID 96 111 By similarity.
FT DISULFID 113 122 By similarity.
FT DISULFID 132 143 By similarity.
FT DISULFID 139 153 By similarity.
FT DISULFID 155 168 By similarity.
FT DISULFID 176 303 By similarity.
FT DISULFID 200 205 By similarity.
FT DISULFID 219 235 By similarity.
FT DISULFID 351 370 By similarity.
FT DISULFID 381 409 By similarity.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 76 76 4-carboxyglutamate (By similarity).
FT MOD_RES 104 104 3-hydroxyaspartate (By similarity).
FT CARBOHYD 186 186 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 244 244 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 446 AA; 50399 MW; 292985BF119C0AA CRC64;

Query Match 47.2%; Score 93.5; DB 1; Length 446;

Best Local Similarity 48.9%; Pred. No. 1.e-07;
Matches 22; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLPGSLXRXCOOCFSXXARXIFKDAKRTLFWISY 45
Db 42 ANS-LLEELWSSSLRECNERSFEAREIFKSPERTQFWIY 85

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.6	44	3 US-08-955-636-3	Sequence 3, Appli
2	161.5	81.6	44	4 US-08-302-239-3	Sequence 3, Appli
3	161.5	81.6	44	3 US-08-397-511-3	Sequence 3, Appli
4	161.5	81.6	44	3 US-08-803-810-3	Sequence 3, Appli
5	161.5	81.6	406	1 US-08-293-778-24	Sequence 24, Appli
6	161.5	81.6	406	1 US-08-395-411-5	Sequence 5, Appli
7	161.5	81.6	406	4 US-08-955-417-1	Sequence 5, Appli
8	161.5	81.6	406	4 US-08-782-587B-1	Sequence 5, Appli
9	161.5	81.6	406	4 US-09-782-587B-3	Sequence 1, Appli
10	161.5	81.6	406	5 PCT-US20-10242-5	Sequence 5, Appli
11	161.5	81.6	444	1 US-08-475-845-2	Sequence 2, Appli
12	161.5	81.6	444	2 US-08-327-650-2	Sequence 2, Appli
13	161.5	81.6	444	2 US-08-660-239-2	Sequence 2, Appli
14	161.5	81.6	444	2 US-08-537-807-2	Sequence 2, Appli
15	161.5	81.6	444	2 US-08-871-003-2	Sequence 2, Appli
16	161.5	81.6	444	3 US-08-464-233-2	Sequence 2, Appli
17	161.5	81.6	444	3 US-09-189-607-2	Sequence 2, Appli
18	161.5	81.6	444	3 US-09-318-907-2	Sequence 2, Appli
19	161.5	81.6	444	5 PCT-US20-05779-2	Sequence 2, Appli
20	161.5	81.6	461	4 US-09-949-016-8819	Sequence 8839, Appli
21	161.5	81.6	466	1 US-08-682-202A-4	Sequence 4, Appli
22	161.5	81.6	466	1 US-08-021-615A-4	Sequence 4, Appli
23	161.5	81.6	466	1 US-08-321-777-4	Sequence 4, Appli
24	161.5	81.6	466	3 US-09-009-217-14	Sequence 14, Appli
25	161.5	81.6	466	3 US-09-009-656-14	Sequence 14, Appli
26	161.5	81.6	466	5 PCT-US20-04193-4	Sequence 4, Appli
27	161.5	81.6	483	4 US-09-949-016-9523	Sequence 9523, Appli

NAME/KEY: MOD_RES
 LOCATION: (0) ... (0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-302-239-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
 Best Local Similarity 97.8%; Pred. No. 5.8e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCXXQCSPXXARXIFKDAVRTKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCXXQCSPXXARXIFKDAVRTKLFWISY 44

RESULT 5

US-08-293-778-24

Sequence 24, Application US/08293778

Patent No. 5580560

GENERAL INFORMATION:
 APPLICANT: Nicolaisen, Elsie M.
 ADDRESS: No. 5580560 No. 5580560th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/293,778
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/104,509
 FILING DATE:
 APPLICATION NUMBER: DK 3235/87
 FILING DATE: 25-JUN-1987
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/434,149
 FILING DATE: 13-NOV-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK88/00103
 FILING DATE: 24-JUN-1988
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/898,248
 FILING DATE: 12-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Aspis, Cheryl H.
 REGISTRATION NUMBER: 34,086
 REFERENCE/DOCKET NUMBER: 3129.224-US

GENERAL INFORMATION:
 APPLICANT: Nelessuen, Gary L.
 TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001
 CURRENT APPLICATION NUMBER: US/09/803,810
 CURRENT FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: fastSSQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 44

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (0) ... (0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-497-591-3

Query Match 81.6%; Score 161.5; DB 4; Length 44;
 Best Local Similarity 97.8%; Pred. No. 5.8e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCXXQCSPXXARXIFKDAVRTKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCXXQCSPXXARXIFKDAVRTKLFWISY 44

RESULT 4

US-08-03-810-3

Sequence 3, Application US/09803810

Patent No. 6762286

GENERAL INFORMATION:
 APPLICANT: Nelessuen, Gary L.
 TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

FILE REFERENCE: 09531/002001
 CURRENT APPLICATION NUMBER: US/09/803,810
 CURRENT FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: fastSSQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 44

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (0) ... (0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-803-810-3

Query Match 81.6%; Score 161.5; DB 1; Length 406;
 Best Local Similarity 75.6%; Pred. No. 5.8e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLRXCXXQCSPXXARXIFKDAVRTKLFWISY 45
 Db 1 ANA-FLTYLRPGSLYRCKYYQCSFYARYIFDAYTKLFWISY 44

RESULT 6
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods for Inhibiting Coagulation

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 81.6%; Score 161.5; DB 1; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

RESULT 8
US-09-782-587B-1
Sequence 1, Application US/09782587B
Patent No. 6806063
GENERAL INFORMATION:
APPLICANT: PEDERSEN, ANDERS H.

APPLICANT: BORNAE, CLAUS
APPLICANT: ANDERSON, KIM V.
FILE REFERENCE: 31-001100US
CURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2002-03-26

RESULT 7
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5668751
GENERAL INFORMATION:

Query 1 ANAGFLXXKRPGSVLRXXXQCSFXARXIFKDAKRTKLFWIISY 45
Database 1 ANA-FLEELRPGSLRECKEQQSFEAREIFKDAERTKLFWIISY 44

Query 1 ANAGFLXXKRPGSVLRXXXQCSFXARXIFKDAKRTKLFWIISY 45
Database 1 ANA-FLEELRPGSLRECKEQQSFEAREIFKDAERTKLFWIISY 44

APPLICANT: Griffin, John H.
APPLICANT: Nesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods and
GENERAL INFORMATION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5
Query Match 81.6%; Score 161.5; DB 2; Length 406;
Best Local Similarity 75.6%; Pred. No. 5.8e-19;
Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

; PRIOR APPLICATION NUMBER: PA 2000 00218
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/184,036
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/241,916
 ; PRIOR FILING DATE: 2000-10-18
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (6) - (7)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (14)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (16)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (19) - (20)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (25) - (26)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (29)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; NAME/KEY: MOD_RES
 ; LOCATION: (35)
 ; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 ; US-09-782-587/B-1
 ; Query Match Score 161.5; DB 4; Length 406;
 ; Best Local Similarity 97.8%; Pred. No. 5.8e-19;
 ; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 ;
 Qy 1 ANAGFLXXLRPGSLRXCXQCSFXXARXIFKDAKXKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCXQCSFXXARXIFKDAKXKLFWISY 44

RESULT 10
 PCT-US92-10242-5
 ; Sequence 5, Application PC/TUS9210242
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffen, John H.
 ; APPLICANT: Masters, Rolf
 ; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods
 ; TITLE OF INVENTION: Anti-Protease-Derived Polypeptides and Therapeutic Methods
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute
 ; STREET: 10661 North Torrey Pines Road, TPC 8
 ; CITY: La Jolla
 ; STATE: CA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOSS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/10242
 ; FILING DATE: 1992/11/18
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/793,989
 ; FILING DATE: 18-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34-163
 ; REFERENCE/DOCKET NUMBER: SCRO472P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-554-2937
 ; TELEFAX: 619-554-6312
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 406 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: Region
 ; LOCATION: 1..152
 ; OTHER INFORMATION: /note= "Factor VII Light Chain"
 ; PCT-US92-10242-5

Query Match Score 161.5; DB 5; Length 406;
 Best Local Similarity 75.6%; Pred. No. 5.8e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

RESULT 9
 US-09-782-587B-3
 ; Sequence 3, Application US/09782587B
 ; Patent No. 6806063
 ; GENERAL INFORMATION:
 ; APPLICANT: PEDERSEN, ANDERS H.
 ; APPLICANT: ANDERSON, KIM V.
 ; APPLICANT: BORNAN, CLAUS
 ; TITLE OF INVENTION: FACTOR VII OR VIA-LIKE MOLECULES
 ; FILE REFERENCE: 31-001100US
 ; CURRENT APPLICATION NUMBER: US/09/782,587B
 ; CURRENT FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: PA 2000 00218
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/184,036
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/241,916
 ; PRIOR FILING DATE: 2000-10-18
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 3
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-782-587B-3

Query Match Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 5.8e-19;

RESULT 11
 US-08-475-B45-2

Sequence 2, Application US/08475845
 ; Patent No. 5788965
 ; GENERAL INFORMATION:
 ; APPLICANT: Berkner, Kathleen L.
 ; APPLICANT: Petersen, Lars C.
 ; APPLICANT: Harr, Charles E.
 ; APPLICANT: Hedner, Ulla
 ; APPLICANT: Bregengaard, Claus
 ; TITLE OF INVENTION: Modified Factor VII
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Street Tower
 ; CITY: San Francisco
 ; STATE: CA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/327,690
 ; FILING DATE: 24-OCT-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/065,725
 ; FILING DATE: 21-MAY-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/662,920
 ; FILING DATE: 28-FEB-1991
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-8-3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-467-9600
 ; TELEFAX: 415-541-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 444 amino acid
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-327-690-2

Query Match Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 6.3e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXQCSXXARXIPDAKRTKLFWISY 45
 Db 39 ANA-FLEELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 82

RESULT 12
 US-08-475-845-2

Query Match Score 161.5; DB 1; Length 444;
 Best Local Similarity 75.6%; Pred. No. 6.3e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXQCSXXARXIPDAKRTKLFWISY 45
 Db 39 ANA-FLEELRPGSLERECKEEQCSFEAREIFKDAERTKLFWISY 82

RESULT 13
 US-08-660-289-2

Sequence 2, Application US/08660289
 ; Patent No. 5833982
 ; GENERAL INFORMATION:
 ; APPLICANT: Berkner, Kathleen L.
 ; APPLICANT: Petersen, Lars C.
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Bregengaard, Claus
 ; TITLE OF INVENTION: Modified Factor VII
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Street Tower
 ; CITY: San Francisco
 ; STATE: CA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660,289
 FILING DATE: 08/06/2003
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/475,845
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION NUMBER: 08/327,690
 FILING DATE: 28-FEB-1991
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REFERENCE/DOCKET NUMBER: 13952-8-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-667-9600
 TELEXFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-660-289-2

Query Match 81.6%; Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 6.3e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAGFLXXLRPGSLXRCKXQCSFXKARXIFKDAVRTKLFWI SY 45
 Db 39 ANA-FLEELRPGSLERKEEQCSFEAREIFDAERTKLFWI SY 82

RESULT 14
 US-08-537-807-2
 ; Sequence 2, Application US/08537807
 ; Patent No. 5861374
 ; GENERAL INFORMATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: Modified Factor VII
 ; NUMBER OF SEQUENCES: 4
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/871,003
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIORITY APPLICATION DATA:
 ; REFERENCE/DOCKET NUMBER: 90-07C7
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 444 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-871-003-2

Query Match 81.6%; Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 6.3e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAGFLXXLRPGSLXRCKXQCSFXKARXIFKDAVRTKLFWI SY 45
 Db 39 ANA-FLEELRPGSLERKEEQCSFEAREIFDAERTKLFWI SY 82

Search completed: August 22, 2005, 18:47:55
 Job time : 30 secs

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 18:45:49 ; Search time 662 Seconds
26.618 Million cell updates/sec (without alignments)

Title: US10031005-3G4

Perfect score: 198

Sequence: 1 ANARGFLXXLRPGSLXRXCKX.....XXARXIFKDAXRTKLFWISY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Published Applications AA:
 1: /cgn2_6/podata/1/pubpaas/us07_PUBCOMB_pep:
 2: /cgn2_6/podata/1/pubpaas/PCT_NEW_PUB_pep:
 3: /cgn2_6/podata/1/pubpaas/us06_NEW_PUB_pep:
 4: /cgn2_6/podata/1/pubpaas/us05_PUBCOMB_pep:
 5: /cgn2_6/podata/1/pubpaas/us04_PUBCOMB_pep:
 6: /cgn2_6/podata/1/pubpaas/PCTUS_PUBCOMB_pep:
 7: /cgn2_6/podata/1/pubpaas/us03_NEW_PUB_pep:
 8: /cgn2_6/podata/1/pubpaas/us02_PUBCOMB_pep:
 9: /cgn2_6/podata/1/pubpaas/us09A_PUBCOMB_pep:
 10: /cgn2_6/podata/1/pubpaas/us08_PUBCOMB_pep:
 11: /cgn2_6/podata/1/pubpaas/us09C_PUBCOMB_pep:
 12: /cgn2_6/podata/1/pubpaas/us05_NEW_PUB_pep:
 13: /cgn2_6/podata/1/pubpaas/us10A_PUBCOMB_pep:
 14: /cgn2_6/podata/1/pubpaas/us10B_PUBCOMB_pep:
 15: /cgn2_6/podata/1/pubpaas/us10C_PUBCOMB_pep:
 16: /cgn2_6/podata/1/pubpaas/us10D_PUBCOMB_pep:
 17: /cgn2_6/podata/1/pubpaas/us10E_PUBCOMB_pep:
 18: /cgn2_6/podata/1/pubpaas/us10F_NEW_PUB_pep:
 19: /cgn2_6/podata/1/pubpaas/us11A_PUBCOMB_pep:
 20: /cgn2_6/podata/1/pubpaas/us11B_NEW_PUB_pep:
 21: /cgn2_6/podata/1/pubpaas/us60A_NEW_PUB_pep:
 22: /cgn2_6/podata/1/pubpaas/us60_B_PUBCOMB_pep:
 RESULT 1
 US-09-803-810-3 ; Application US/09803810
 ; Sequence 3, Application US/09803810
 ; Publication No. US20010018414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nelsetuen, Gary L.
 ; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
 ; POLYPEPTIDES
 ; FILE REFERENCE: 19531/02001
 ; CURRENT APPLICATION NUMBER: US/09/803,810
 ; CURRENT FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 3
 ; LENGTH: 44
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD RES
 ; LOCATION: (0) .. (0)
 ; OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

Summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.6	44	9 US-09-803-810-3	Sequence 3, Appli
2	161.5	81.6	44	14 US-10-298-330-3	Sequence 3, Appli
3	161.5	81.6	44	16 US-10-855-068-3	Sequence 3, Appli
4	161.5	81.6	406	10 US-09-7587B-1	Sequence 1, Appli
5	161.5	81.6	406	14 US-09-7887B-3	Sequence 3, Appli
6	161.5	81.6	406	14 US-10-109-498-1	Sequence 1, Appli
7	161.5	81.6	406	14 US-10-255-032-1	Sequence 1, Appli
8	161.5	81.6	406	14 US-10-281-127-1	Sequence 1, Appli
9	161.5	81.6	406	15 US-10-386-898-7	Sequence 7, Appli
10	161.5	81.6	406	15 US-10-383-898-1	Sequence 1, Appli
11	161.5	81.6	406	15 US-10-617-500-1	Sequence 1, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.6	44	9 US-09-803-810-3	Sequence 3, Appli
2	161.5	81.6	44	14 US-10-298-330-3	Sequence 3, Appli
3	161.5	81.6	44	16 US-10-855-068-3	Sequence 3, Appli
4	161.5	81.6	406	10 US-09-7587B-1	Sequence 1, Appli
5	161.5	81.6	406	14 US-09-7887B-3	Sequence 3, Appli
6	161.5	81.6	406	14 US-10-109-498-1	Sequence 1, Appli
7	161.5	81.6	406	14 US-10-255-032-1	Sequence 1, Appli
8	161.5	81.6	406	14 US-10-281-127-1	Sequence 1, Appli
9	161.5	81.6	406	15 US-10-386-898-7	Sequence 7, Appli
10	161.5	81.6	406	15 US-10-383-898-1	Sequence 1, Appli
11	161.5	81.6	406	15 US-10-617-500-1	Sequence 1, Appli

Query Match 81.6%; Score 161.5; DB 9; Length 44;
 Best Local Similarity 97.8%; Pred. No. 1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCKXQCSFXARXIFKDXRTKLFWISY 45
 Db 1 ANA-FLXXLRPGSLXRXCKXQCSFXARXIFKDXRTKLFWISY 44

RESULT 2
 US-10-298-330-3

Sequence 3, Application US/10299330
; GENERAL INFORMATION:
; APPLICANT: Neelsetuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6..7, 14..16, 19..20, 25..26, 29..35
; OTHER INFORMATION: xaa = gamma carboxyglutamic acid or glutamic acid
; US-10-298-330-3

Query Match 81.6%; Score 161.5; DB 14; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAGFLXXLRPGSLRXCXQCSFXXARXIFKDAKRTKLFWIISY 45
1 ANA-FLXXLRPGSLRXCXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 3
US-10-855-068-3
; Sequence 3, Application US/10855068
; GENERAL INFORMATION:
; APPLICANT: Neelsetuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 09531-002601
; CURRENT APPLICATION NUMBER: US/10/855,068
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US/09/302,239
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid
; US-10-855-068-3

Query Match 81.6%; Score 161.5; DB 16; Length 44;
Best Local Similarity 97.8%; Pred. No. 1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAGFLXXLRPGSLRXCXQCSFXXARXIFKDAKRTKLFWIISY 45
1 ANA-FLXXLRPGSLRXCXQCSFXXARXIFKDAKRTKLFWIISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAEAS, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19

RESULT 4
US-09-782-587B-1
; Sequence 1, Application US/09782587B

SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match 81.6%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCQCSXXARXIFKDAKRTKLFWIISY 45
Db 1 ANA-FLXXLRPGSLXRXCQCSXXARXIFKDAKRTKLFWIISY 44

RESULT 8
US-10-255-032-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Person, Egon
; APPLICANT: Olsen, Ole Hviilsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; PRIOR APPLICATION NUMBER: PA 2001 016227
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)

US-10-255-032-1
; Sequence 1, Application US/1010498
; Publication No. US20030044308A1
; GENERAL INFORMATION:
; APPLICANT: Person, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6486 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-32
; PRIOR APPLICATION NUMBER: 60/211,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match 81.6%; Score 161.5; DB 14; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAGFLXXLRPGSLXRXCQCSXXARXIFKDAKRTKLFWIISY 45
Db 1 ANA-FLXXLRPGSLXRXCQCSXXARXIFKDAKRTKLFWIISY 44

RESULT 9
US-10-386-898-7
; Sequence 7, Application US/10386898
; Publication No. US20030229018A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030229018A1 No. US20030229018A1
; APPLICANT: Kjalle, Marianne
; APPLICANT: Jakobsen, Palle
; APPLICANT: Stennicke, Henning Ralf
; TITLE OF INVENTION: DIMERIC TF ANTAGONIST
; FILE REFERENCE: 6415.200-US
; CURRENT APPLICATION NUMBER: US/10/386,898
; PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/365,935
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

RESULT 7
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A1 No. US20030100075A1
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357.WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; PRIOR APPLICATION NUMBER: 2002-09-24
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-386-898-7

Query Match 81.6%; Score 161.5; DB 15; Length 406;
 Best Local Similarity 97.8%; Pred. No. 9.1e-19;
 Matches 44; Conservative 0; Mismatches 0;
 Indels 1; Gaps 1;

Qy 1 ANAGFLXXLPGSLXRXCXXQCSPXXAXKIFDAKRTKLFWI SY 45
 Db 1 ANA-FLEELRPGSLERCKEQQCSPEEARIFKDAERTKLFWI SY 44

RESULT 11
 US-10-617-500-1

; Sequence 1, Application US/10617500
 ; Publication No. US20040072755A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Novo Nordisk Pharmaceuticals, Inc.
 ; FILE REFERENCE: 6510-200-US
 ; CURRENT APPLICATION NUMBER: US10/617,500
 ; CURRENT FILING DATE: 2003-07-11
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CHAIN
 ; LOCATION: (1) .. (406)

Query Match 81.6%; Score 161.5; DB 15; Length 406;
 Best Local Similarity 75.6%; Pred. No. 9.1e-19;
 Matches 34; Conservative 0; Mismatches 10;
 Indels 1; Gaps 1;

Qy 1 ANAGFLXXLPGSLXRXCXXQCSPXXAXKIFDAKRTKLFWI SY 45
 Db 1 ANA-FLEELRPGSLERCKEQQCSPEEARIFKDAERTKLFWI SY 44

RESULT 12
 US-10-263-205B-2

; Sequence 2, Application US/10263205B
 ; Publication No. US20040087498A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERKNER, Kathleen L.
 ; APPLICANT: PETERSEN, Lars
 ; APPLICANT: HART, Charles E.
 ; APPLICANT: HEDNER, Ulla
 ; APPLICANT: BREGENGAARD, Claus
 ; TITLE OF INVENTION: MODIFIED FACTOR VII
 ; FILE REFERENCE: 13952N-8-5-1
 ; CURRENT APPLICATION NUMBER: US/10/263, 205B
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 081464, 029
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: 081327, 690
 ; PRIOR FILING DATE: 1994-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US94/05779
 ; PRIOR FILING DATE: 1994-05-23
 ; PRIOR APPLICATION NUMBER: 081065, 725
 ; PRIOR FILING DATE: 1993-05-21
 ; PRIOR APPLICATION NUMBER: PCT/US92/01636
 ; PRIOR FILING DATE: 1991-02-28
 ; PRIOR APPLICATION NUMBER: 071662, 920
 ; PRIOR FILING DATE: 1991-02-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 2
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-263-205B-2

Query Match 81.6%; Score 161.5; DB 15; Length 406;
 Best Local Similarity 97.8%; Pred. No. 9.1e-19;
 Matches 44; Conservative 0; Mismatches 0;
 Indels 1; Gaps 1;

Qy 1 ANAGFLXXLPGSLXRXCXXQCSPXXAXKIFDAKRTKLFWI SY 45
 Db 1 ANA-FLEELRPGSLERCKEQQCSPEEARIFKDAERTKLFWI SY 44

RESULT 13
 US-10-617-619-1

; Sequence 1, Application US/10617619
 ; Publication No. US20040110923A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicolaisen, Else M
 ; APPLICANT: Jorgensen, Anker S
 ; TITLE OF INVENTION: TF Binding Compound
 ; FILE REFERENCE: 6455-200-US
 ; CURRENT APPLICATION NUMBER: US/10/617,619
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
 ; PRIOR FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (1) .. (406)
 ; OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-617-500-1

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1) ..(406)
; OTHER INFORMATION: xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-617-619-1

Query Match 81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1;
Gaps 1;
OTHER INFORMATION: xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1

Search completed: August 22, 2005, 19:20:43
Job time : 662 secs

RESULT 14
; Sequence 1, Application US/10701294
; Publication No. US2004143039A1
; GENERAL INFORMATION:
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
; APPLICANT: Petersen, Lars C
; APPLICANT: Back, Jacob M
; APPLICANT: Meyer, Christian
; TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
; FILE REFERENCE: 6608 200-US
; CURRENT APPLICATION NUMBER: US10/701,294
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: US 60/434,904
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01770
; PRIOR FILING DATE: 2002-11-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1) ..(406)
; OTHER INFORMATION: xaa=4-carboxyglutamic acid (Gamma-carboxyglutamate)
US-10-701-294-1

Query Match 81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1;
Gaps 1;
OTHER INFORMATION: xaa=4-carboxyglutamic acid (Gamma-carboxyglutamate)
US-10-669-537-1

Query Match 81.6%; Score 161.5; DB 16; Length 406;
Best Local Similarity 97.8%; Pred. No. 9.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1;
Gaps 1;
OTHER INFORMATION: xaa=carboxyglutamic acid (gamma-carboxyglutamate)
US-10-669-537-1

Search completed: August 22, 2005, 19:20:43
Job time : 662 secs

RESULT 15
; Sequence 1, Application US/10669537
; Publication No. US2004192602A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Ole Hvilsted
; TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
; FILE REFERENCE: 6544 200-US
; CURRENT APPLICATION NUMBER: US10/669,537
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US 60/417,927
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 13

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:28:04 ; Search time 92 Seconds
(without alignments)

189.176 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: ANAYFLXXLRPGSLXRXCKX.....XXARXIFKDAKRTKLFWIY 45

Scoring table: BL0SUM62

Gapext 0.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : A_Geneseqp_16Dec04:*

- 1: Geneseqp_1980s:*
- 2: Geneseqp_1990s:*
- 3: Geneseqp_2000s:*
- 4: Geneseqp_2001s:*
- 5: Geneseqp_2002s:*
- 6: Geneseqp_2003ab:*
- 7: Geneseqp_2003bs:*
- 8: Geneseqp_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	169	84.9	408	7 ADF44980	Adf44980 Human Fac
2	161.5	81.2	44	2 AAY18305	Aay18305 Human Fac
3	161.5	81.2	44	4 AAB36395	Aab36395 Human Fac
4	161.5	81.2	44	7 ADD50096	Add50096 Human Fac
5	161.5	81.2	44	8 ADO26902	Adg26902 Human Fac
6	161.5	81.2	401	4 AAB84870	Aab84870 Mutant b1
7	161.5	81.2	401	4 AAB84871	Aab84871 Mutant b1
8	161.5	81.2	406	2 AAR35764	Aar35764 Factor VII
9	161.5	81.2	406	2 AAW14510	AAw14510 Modified
10	161.5	81.2	406	2 AAW14509	AAw14509 Modified
11	161.5	81.2	406	4 AAU7745	Aau7745 Human fac
12	161.5	81.2	406	4 AAB84867	Aab84867 Mutant b1
13	161.5	81.2	406	4 AAB84868	Aab84868 Mutant b1
14	161.5	81.2	406	4 AAB84869	Aab84869 Mutant b1
15	161.5	81.2	406	4 AAB84866	Aab84866 Wild-type
16	161.5	81.2	406	4 AAM52183	Aam52183 Human FVII
17	161.5	81.2	406	4 AAM52172	Aam52172 Mammalian
18	161.5	81.2	406	4 AAM52166	Aam52166 Human FVI
19	161.5	81.2	406	4 AAM52171	Aam52171 Human FVI
20	161.5	81.2	406	4 AAM52187	Aam52187 Human FVI
21	161.5	81.2	406	4 AAM52181	Aam52181 Human FVI
22	161.5	81.2	406	4 AAM52185	Aam52185 Human FVI
23	161.5	81.2	406	4 AAM52184	Aam52184 Human FVI
24	161.5	81.2	406	4 AAM52182	Aam52182 Human FVI
25	161.5	81.2	406	5 AAU77196	Aau77196 Human coa

ALIGNMENTS

RESULT 1
ID ADF44980 standard; protein; 408 AA.

XX AC ADF44980;
XX DT 12-FEB-2004 (first entry)
XX DE Human Factor VII variant, AAY.
XX KW Human; Factor VII; FVII; Factor VIIa; blood coagulation factor;
KW blood clotting disorder; brain haemorrhage; trauma; bleeding;
KW Haemostatic.
XX OS Synthetic.
XX OS Homo sapiens.

FH Key Misc-difference 4. -5
FT FT /note= "Residues AY were inserted after position 3"
XX WO2003093465-A1.

FT XX WO2003093465-A1.

XX PD 13-NOV-2003.

XX PR 29-APR-2003; 2003WO-DK000276.

XX PR 30-APR-2002; 2002US-0376679P.

XX PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.

PI Haaning JM, Andersen KV, Pedersen AH;

XX DR 2003-903672/82.

XX PT New Factor VII (FVII) or Factor VIIa polypeptide variant, useful in preparing a composition for treating a disorder where clot formation is desirable, e.g., brain hemorrhages or blunt or penetrative trauma.

CC CC The present invention relates to novel variants of Factor VII (FVII) or Factor VII (FVIIa) protein. FVII is a blood coagulation factor. The present sequence is a variant of the invention. The variants are useful in preparing a composition for treating a disorder where clot formation is desirable, e.g., brain hemorrhages, blunt or penetrative trauma, bleeding in patients undergoing living transplants or resection or

Claim 13, Page 78pp; English.

CC variceal bleedings. Note: The present sequence is not shown in the
 CC specification, but was derived from information given in the wild-type
 CC human FVII sequence (ADP44971) and Claim 13.

XX SQ Sequence 408 AA;
 XX Query Match 84.9%; Score 169; DB 7; Length 408;
 Best Local Similarity 76.7%; Pred. No. 3.6e-20;
 Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 XX QY 3 AYFLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 45
 Db 4 AYPLBLRPPSLERKECKBGSFEEAREIFKDABRTKLFWIISY 46
 XX KW Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX DT 27-FEB-2001 (first entry)
 XX AC AAB36395;
 XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX DE Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 XX DE Gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 XX DE Factor X; prothrombin; enhanced membrane binding affinity;
 XX DE clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
 XX DE clotting disorder; haemophilia A; haemophilia B; liver disease.
 XX OS Homo sapiens.
 XX PN WO200066753-A2.
 XX PD 09-NOV-2000.
 XX PF 28-APR-2000; 2000WO-US011116.
 XX PR 29-APR-1999; 99US-00302239.
 XX PA (MINU) UNIV MINNESOTA.
 XX PI Nelsestuen GL;
 XX DR WPI; 2001-007226/01.
 XX PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and haemophilia, comprises modified gamma-
 PT carboxy glutamic acid domain that enhances membrane binding affinity.
 XX Disclosure: Page 12; 81pp; English.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 1..44
 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
 acid"
 XX FT AT WO9920767-A1.
 XX PD 29-APR-1999.
 XX PF 20-OCT-1998; 98WO-US022152.
 XX PR 23-OCT-1997; 97US-00955636.
 XX PA (MINU) UNIV MINNESOTA.
 XX PI Nelsestuen GL;
 XX DR WPI; 1999-288309/24.
 XX PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid
 PT domain, useful for treating clotting disorders.
 XX PS Sequence 15; 80pp; English.
 XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid) domain.
 CC The invention relates to a vitamin K-dependent polypeptide comprising a
 CC modified GLA domain containing an amino acid substitution which enhances
 CC membrane binding of the modified polypeptide as compared to the native
 CC polypeptide. The polypeptide is used to treat a clotting disorder by
 CC decreasing or increasing clot formation. Modification of the GLA domain
 CC results in a protein which has enhanced membrane binding affinity as
 CC compared to the native protein
 XX SQ Sequence 44 AA;

XX Query Match 81.2%; Score 161.5; DB 2; Length 44;
 Best Local Similarity 9.8%; Pred. No. 7.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 XX QY 1 ANAVFLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 45
 Db 1 ANA-FLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 44
 XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX Disclosure: Page 12; 81pp; English.

XX SQ Sequence 44 AA;
 XX Query Match 81.2%; Score 161.5; DB 4; Length 44;
 Best Local Similarity 9.8%; Pred. No. 7.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 XX QY 1 ANAVFLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 45
 Db 1 ANA-FLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 44
 XX DE Human vitamin K-dependent protein #2.
 XX Disclosure: Page 12; 81pp; English.

RESULT 3
 ID AAB36395 standard; peptide: 44 AA.
 XX AC AAB36395;
 XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX DT 27-FEB-2001 (first entry)
 XX AC AAB36395;
 XX DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
 XX DE Vitamin K-dependent protein; factor VII; protein C; GLA domain;
 XX DE Gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
 XX DE Factor X; prothrombin; enhanced membrane binding affinity;
 XX DE clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis;
 XX DE clotting disorder; haemophilia A; haemophilia B; liver disease.
 XX OS Homo sapiens.
 XX PN WO200066753-A2.
 XX PD 09-NOV-2000.
 XX PF 28-APR-2000; 2000WO-US011116.
 XX PR 29-APR-1999; 99US-00302239.
 XX PA (MINU) UNIV MINNESOTA.
 XX PI Nelsestuen GL;
 XX DR WPI; 2001-007226/01.
 XX PT Novel vitamin K-dependent polypeptide useful for treating clotting
 PT disorders such as thrombosis and haemophilia, comprises modified gamma-
 PT carboxy glutamic acid domain that enhances membrane binding affinity.
 XX Disclosure: Page 12; 81pp; English.

PS Sequence 44 AA;

XX Query Match 81.2%; Score 161.5; DB 4; Length 44;
 Best Local Similarity 9.8%; Pred. No. 7.2e-20;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 XX QY 1 ANAVFLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 45
 Db 1 ANA-FLXXLRPSSLXRXCKXXXCSFXKARXIFKDAXRTKLFWIISY 44
 XX DE Human vitamin K-dependent protein #2.
 XX Disclosure: Page 12; 81pp; English.

RESULT 4
 ID ADD50096 standard; peptide: 44 AA.
 XX AC ADD50096;
 XX DE Human vitamin K-dependent protein #2.
 XX Disclosure: Page 12; 81pp; English.

XX (KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.
 PA WPI; 2001-310677/33.
 DR N-PSDB; AAH19463.
 XX Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX Claim 14; Page 20-21; 29pp; Japanese.
 XX The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-31. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.
 XX Sequence 401 AA;
 Query Match 81.2%; Score 161.5; DB 4; Length 401;
 Best Local Similarity 75.6%; Pred. No. 6.9e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAVFLXXLRPGSLXRCKXXXQCSFXXARXIFKDAKRTKLFWIISY 45
 Db 1 ANA-FLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWIISY 44

RESULT 8
 ID AAR35764 Standard; protein: 406 AA.
 SQ AAR35764:
 XX AC AAR35764;
 XX DT 25-MAR-2003 (revised)
 XX 24-SEP-1993 (first entry)
 DE Factor VII (VIII).
 KW PC; protein C; IX; Factor IX; X; Factor X; PT; prothrombin; VII;
 KW Factor VII; CT; chymotrypsinogen; SP; serine protease; binding; exosite;
 KW catalytic activity.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1 .152
 FT Region /note= "Factor VII light chain"
 FT 153 .406
 FT Peptide /note= "Factor VII heavy chain"
 FT 245 .266
 FT /note= "claim 9, page 138-139 describes an antibody that reacts with Factor VII; fragments 289-304, 290-304, 290-310, 374-388 and 400-414 but not with Fragment 245-266"
 FT Peptide 289 .304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 290 .310
 FT /note= "exosite 2"
 FT Peptide 290 .310
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 FT Peptide 290 .304
 FT /note= "pref. PC polypeptide; claim 4, page 137"
 FT Peptide 374 .388
 FT /note= "exosite 1"
 FT Peptide 374 .388
 FT /note= "pref. PC polypeptide; claim 2, page 136"
 XX PN WO9303804-A1.
 XX PD 27-MAY-1993.
 XX PF 18-NOV-1992; 92WO-US010242.
 XX PR 18-NOV-1991; 91US-00793389.
 XX PA (SCRIPPS) SCRIPPS RES INST.
 XX PI Griffin JH, Masters RM;
 XX DR WPI; 1993-182244/22.
 XX Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples.
 XX Disclosure; Page 133-135; 149pp; English.
 PS The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.
 XX The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-39. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients.
 CC PS Disclosure; Page 133-135; 149pp; English.
 CC The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp.

Page 5

```

PT Disulfide-bond 50. .61
PT Disulfide-bond 55. .70
Modified-site 63
    /label= OTHER
    /note= "beta-hydroxy-aspartic acid"
FT Disulfide-bond 72. .81
FT Disulfide-bond 91. .102
FT Disulfide-bond 98. .112
FT Disulfide-bond 114. .127
FT Disulfide-bond 135. .162
FT Cleavage-site 143. .144
    /note= "proteolytic site"
FT Modified-site 145
    /note= "glycosylation site"
FT Disulfide-bond 159. .164
FT Disulfide-bond 178. .194
FT Active-site 193
FT Active-site 242
FT Cleavage-site 290. .291
    /note= "proteolytic site"
FT Disulfide-bond 310. .329
FT Cleavage-site 315. .316
    /note= "proteolytic site in unmodified protein"
FT Misc-difference 315
    /note= "native Arg315 has been substituted by a proteolytically more stable residue"
FT Modified-site 322
    /note= "glycosylation site"
FT Disulfide-bond 340. .368
FT Cleavage-site 341. .342
    /note= "proteolytic site"
FT Active-site 344
FT Cleavage-site 392. .393
    /note= "proteolytic site"
FT Cleavage-site 396. .397
    /note= "proteolytic site"
FT Cleavage-site 402. .403
    /note= "proteolytic site"
XX US5580560-A.
    /note= "proteolytic site"
XX 03-DEC-1996.
XX 94US-00293778.
XX 22-AUG-1994;
XX 13-NOV-1989;
XX 89US-00431149.
XX 12-JUN-1992;
XX 92US-00898248.
XX 09-AUG-1993;
XX 93US-00104509.
XX (NOVO ) NOVO-NORDISK AS.
XX WPI; 1997-033523/03.
XX Murated human factor VII or VIII proteins - with amide groups to improve proteolytic stability.
XX Example 4; Page; 28pp; English.
XX Sequence 406 AA;
XX

```

Query Match Score 161.5; DB 2; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFPLXXLRPGSLRXCXQCSFXAXRIFKDAKRTKLFWIY 45
 Db 1 ANA-FLEELPGLSERECKEEBQCSPEEARIFKDAKRTKLFWIY 44

RESULT 10
 AAW14509 standard; protein; 406 AA.
 XX
 AC AAW14509;
 XX DT 25-MAR-2003 (revised)
 DT 14-NAY-1997 (first entry)
 DE Modified blood coagulation Factor VII (R290S).
 XX KW Blood coagulation; factor 7; mutein; mutation; modification;
 KW thrombocytopenia; von Willebrand's disease; plasma substitute.
 XX OS Homo sapiens.
 XX Synthetic.
 FH Key Location/Qualifiers
 FT Modified site 6
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 7
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 14
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 16
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Disulfide-bond 17 .22
 FT Modified site 19
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 20
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 25
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 26
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified site 29
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 32 .33
 FT Modified site 35
 FT /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 38 .39
 FT Cleavage-site 42 .43
 FT Cleavage-site 44 .45
 FT Disulfide-bond 50 .61
 FT Disulfide-bond 55 .70
 FT Modified site 63
 FT /note= "proteolytic site"
 FT Disulfide-bond 72 .81
 FT Disulfide-bond 91 .102

FT FT Disulfide-bond 98 .112
 FT FT Disulfide-bond 114 .127
 FT FT Disulfide-bond 135 .162
 FT FT Cleavage-site 143 .144
 FT FT /note= "proteolytic site"
 FT FT Modified-site 145
 FT FT /note= "glycosylation site"
 FT FT Disulfide-bond 159 .164
 FT FT Disulfide-bond 178 .194
 FT FT Active-site 193
 FT FT Active-site 242
 FT FT Cleavage-site 290 .291
 FT FT /note= "proteolytic site in unmodified factor VII"
 FT FT Misc-difference 290
 FT FT /note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
 FT FT Disulfide-bond 310 .329
 FT FT Cleavage-site 315 .316
 FT FT /note= "proteolytic site"
 FT FT Modified-site 322
 FT FT Disulfide-bond 340 .368
 FT FT Cleavage-site 341 .342
 FT FT Active-site 344
 FT FT Cleavage-site 392 .393
 FT FT /note= "proteolytic site"
 FT FT Cleavage-site 396 .397
 FT FT /note= "proteolytic site"
 FT FT Cleavage-site 402 .403
 FT FT /note= "proteolytic site"
 XX US5580560-A.
 XX PD 03-DEC-1996.
 XX PF 22-AUG-1994; 94US-00293778.
 XX PR 13-NOV-1989; 89US-00434149.
 PR 12-JUN-1992; 92US-00898448.
 PR 09-AUG-1993; 93US-00104509.
 XX (NOVO) NOVO-NORDISK AS.
 XX PI Wiberg FC, Woodbury R, Nicolaisen EM, Bjorn SE;
 XX DR WPI; 1997-013523/03.
 XX PT Mutated human factor VII or VIIa proteins - with amino acid substitutions to improve proteolytic stability.
 XX PS Example 3: Page: 28pp; English.
 XX CC Modified human factor VII or VIIa proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32, Lys38, Lys42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and Lys341 by an amino acid that provides a proteolytically more stable peptide bond,
 CC provided that Lys32 is replaced by Gln, Glu, His, Gly, Thr, Ala or Ser.
 CC The modified proteins are useful for treating bleeding disorders such as thrombocytopenia and von Willebrand's disease. They are also suitable for addition to plasma substitutes. The present sequence is a specific example of a modified factor VII protein. (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 406 AA;
 Query Match Score 161.5; DB 2; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFPLXXLRPGSLRXCXQCSFXAXRIFKDAKRTKLFWIY 45
 Db 1 ANA-FLEELPGLSERECKEEBQCSPEEARIFKDAKRTKLFWIY 44

RESULT 11
AAU77745 standard; protein; 406 AA.
 ID AAU77745
 XX
 AC
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human factor VIIa active site mutant.
 XX
 Factor VIIa; human; shock heat treatment; protein stability;
 protein manufacturer; protein conformation; mutant; mutein.
 XX
 KW
 KW
 KU
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Location/Qualifiers
 Key 193
 Active-site /note= "Member of the factor VIIa catalytic triad"
 Active-site 242 /note= "Member of the factor VIIa catalytic triad"
 Misc-difference 344 /label= GLY, Met, Thr
 FT /note= "Preferably Ala. Wild type Ser"
 Active-site 344 /note= "Member of the factor VIIa catalytic triad"
 FT
 XX WO201177141-A1.
 PN
 XX
 PD 18-OCT-2001.
 XX
 PP 06-APR-2001; 2001WO-DK000234.
 XX 06-APR-2000; 2000DK-00000573.
 PR 17-APR-2000; 2000US-0197650P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PS
 XX
 PI
 XX
 DR WPI; 2001-65162/75.
 XX
 PT Stabilization of a polypeptide e.g. in a pharmaceutical composition
 PT involves a shock heat treatment.
 XX
 Disclosure; Page; 22pp; English.
 XX
 CC The invention describes a method of stabilising a polypeptide involving
 CC shock heat treatment of the polypeptide. The method is useful in a
 CC pharmaceutical composition. The method is useful in a
 CC manufacturing a polypeptide, also as a unit operation during preparation,
 CC purification, recovery and/or formulation of polypeptides. The shock heat
 CC treatment improves the protein stability without substantial loss of
 CC biological activity. The method can be applied to change polypeptide
 CC conformation in a very fast and non-invasive manner. The polypeptide
 CC formed is stable. The method is also useful for decreasing the
 CC association of the polypeptide. This sequence represents a modified human
 CC factor VIIa protein, mutated at the catalytic site, described in the
 CC invention. Note: This sequence does not appear in the specification but
 CC has been obtained using information given in the invention
 XX
 Sequence 406 AA;

Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXXQCSPXXAXXIFDAXRTKLFWIWSY 45
 Db 1 ANA-FLEELRPGLSERECKEQCSPEAREIFDAERTKLFWIWSY 44

RESULT 12
AABB8867 standard; protein; 406 AA.
 ID AABB8867
 XX
 AC
 XX
 DT 31-JUL-2001 (First entry)
 XX
 DS Mutant blood coagulant factor VII (FVII-5).
 XX
 DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW
 KW mutant; mutein.
 XX
 OS Homo sapiens.

OS Synthetic.
 XX
 FH Location/Qualifiers
 Key 159
 FT Misc-difference /note= "Wild-type Cys substituted by Ala"
 FT
 FT Misc-difference 164
 FT /note= "Wild-type Cys substituted by Ala"
 PN JP2001061479-A.
 PN
 XX
 PD 13-MAR-2001.
 XX
 PP 24-AUG-1999; 99JUP-00237610.
 XX
 PR 24-AUG-1999; 99JUP-00237610.
 XX
 PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
 XX
 DR WPI; 2001-310677/33.
 DR N-PSMB; AAH19460.
 XX
 PT Mutant of blood coagulant factor VII, used for substitution therapy in
 PT the treatment of hemophilia.
 XX
 PS Claim 3; Page 11-12; 29pp; Japanese.
 XX
 CC The present invention relates to mutants of blood coagulant factor VII
 CC (FVII) or activated blood coagulant factor VII (FVII). The present
 CC sequence is one such mutant FVII: VII-5. In the wild-type protein
 CC (AABB8866), there is a disulphide bond (15Cys-164Cys). In the present
 CC protein, the disulphide bond is disrupted. The mutants can be used as an
 CC agent for the substitution therapy of haemophilia inhibitor patients
 XX
 Sequence 406 AA;

Query Match 81.2%; Score 161.5; DB 4; Length 406;
 Best Local Similarity 75.6%; Pred. No. 7e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXXQCSPXXAXXIFDAXRTKLFWIWSY 45
 Db 1 ANA-FLEELRPGLSERECKEQCSPEAREIFDAERTKLFWIWSY 44

RESULT 13
AABB84868 standard; protein; 406 AA.
 ID AABB84868
 XX
 AC
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Mutant blood coagulant factor VII (FVII-6).
 XX
 KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 KW mutant; mutein.
 XX
 OS Homo sapiens.

OS	Synthetic.		PA	(KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.
XX	Key	Location/Qualifiers	XX	WPI; 2001-310677/33.
FT	Misc-difference 164		DR	N-PSDB; AAH19462.
FT	/note= "Wild-type Cys substituted by Ala"		XX	
FT	Misc-difference 299		PT	Mutant of blood coagulant factor VII, used for substitution therapy in
FT	/note= "Wild-type Val substituted by Cys"		PT	the treatment of hemophilia.
XX	JP2001061479-A.		XX	Claim 9; Page 17-18; 29pp; Japanese.
XX	PD	13-MAR-2001.	XX	The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-30. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients
XX	PP	24-AUG-1999; 99JP-00237610	XX	
XX	PR	24-AUG-1999; 99JP-00237610	XX	
XX	PA	(KAGA) ZH KAGAKU & KESSEI RYOHOKENKYUSHO.	XX	
XX	WPI;	2001-310677/33.	XX	
DR	DR		XX	
XX	PT	Mutant of blood coagulant factor VII, used for substitution therapy in	XX	
XX	PT	the treatment of hemophilia.	XX	
XX	PS	Claim 5; Page 14-15; 29pp; Japanese.	XX	
XX	XX	The present invention relates to mutants of blood coagulant factor VII (FVII) or activated blood coagulant factor VII (FVIIa). The present sequence is one such mutant FVII: VII-6. In the wild-type protein (AA84866), there is a disulphide bond (15Cys-164Cys). In the present protein, the disulphide bond is disrupted. The mutants can be used as an agent for the substitution therapy of haemophilia inhibitor patients	XX	
XX	SQ	Sequence 406 AA;	XX	
XX	Query Match	81.2%; Score 161.5; DB 4; Length 406;	XX	RESULT 15
XX	Best Local Similarity	75.6%; Pred. No. 7e-19; Indels 1; Gaps 1;	XX	AAB84866 standard; protein; 406 AA.
XX	Matches	34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	XX	ID AAB84866
XX	Qy	1 ANAYFLXXLRPGSLXRXCKXXQCSFXAXRKFDAKRTKLFWI SY 45	XX	CC Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
XX	Db	1 ANA-FLEELRPGLSERECKEEQCSFEAREIFKDAERTKLFWI SY 44	XX	AC AAB84866;
XX	XX	Sequence 406 AA;	XX	AC AC
XX	XX	Query Match	81.2%; Score 161.5; DB 4; Length 406;	XX
XX	Best Local Similarity	75.6%; Pred. No. 7e-19; Indels 1; Gaps 1;	XX	DE Wild-type human blood coagulant factor VII (FVII).
XX	Matches	34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	XX	ID AAB84866
XX	Qy	1 ANAYFLXXLRPGSLXRXCKXXQCSFXAXRKFDAKRTKLFWI SY 45	XX	XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia.
XX	Db	1 ANA-FLEELRPGLSERECKEEQCSFEAREIFKDAERTKLFWI SY 44	XX	XX Homo sapiens.
XX	XX	Sequence 406 AA;	XX	XX Homo sapiens.
XX	XX	Query Match	81.2%; Score 161.5; DB 4; Length 406;	XX
XX	Best Local Similarity	75.6%; Pred. No. 7e-19; Indels 1; Gaps 1;	XX	XX Disclosure; Page 8-9; 29pp; Japanese.
XX	Matches	34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	XX	XX
XX	Qy	1 ANAYFLXXLRPGSLXRXCKXXQCSFXAXRKFDAKRTKLFWI SY 45	XX	XX
XX	Db	1 ANA-FLEELRPGLSERECKEEQCSFEAREIFKDAERTKLFWI SY 44	XX	XX
XX	XX	Sequence 406 AA;	XX	XX
XX	XX	Query Match	81.2%; Score 161.5; DB 4; Length 406;	XX
XX	Best Local Similarity	75.6%; Pred. No. 7e-19; Indels 1; Gaps 1;	XX	XX
XX	Matches	34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	XX	XX
XX	Qy	1 ANAYFLXXLRPGSLXRXCKXXQCSFXAXRKFDAKRTKLFWI SY 45	XX	XX
XX	Db	1 ANA-FLEELRPGLSERECKEEQCSFEAREIFKDAERTKLFWI SY 44	XX	XX
XX	XX	Sequence 406 AA;	XX	XX
XX	XX	Query Match	81.2%; Score 161.5; DB 4; Length 406;	XX
XX	Best Local Similarity	75.6%; Pred. No. 7e-19; Indels 1; Gaps 1;	XX	XX
XX	Matches	34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	XX	XX
XX	Qy	1 ANAYFLXXLRPGSLXRXCKXXQCSFXAXRKFDAKRTKLFWI SY 45	XX	XX
XX	Db	1 ANA-FLEELRPGLSERECKEEQCSFEAREIFKDAERTKLFWI SY 44	XX	XX
XX	XX	Sequence 406 AA;	XX	XX

	Qy	Db
1	ANAYPLXXLRPGSLXRXCXQQCSFXMARXIFDAXYKLFWISY 45	
1	ANA FLEELRPGSLRECKEESCSFEEAEIFDAERTLFWISY 44	
1	ANA FLEELRPGSLRECKEESCSFEEAEIFDAERTLFWISY 44	

Search completed: August 22, 2005, 18:45:41
Job time : 93 sec

This Page Blank (uspto)

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using bw model

Run on: August 22, 2005, 09:28:04 ; Search time 25 Seconds
(without alignments)

173.190 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: AAVRYFLXXLRPGSLRXCKX.....XXARXIFKDAVRTKLFWIY 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:
1: _pir1:
2: _pir2:
3: _pir3:
4: _pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	466	1 KPHU7	coagulation factor
2	127.5	64.1	443	2 I46932	coagulation factor
3	113.8	56.8	407	1 KFB07	coagulation factor
4	98.5	49.5	461	1 JX0210	protein C (activat
5	93.5	47.0	456	1 KXBO	protein C (activat
6	91.5	46.0	488	1 EXHU	coagulation factor
7	90.5	45.5	492	1 EXBO	coagulation factor
8	89.5	45.0	461	1 S8994	protein C (activat
9	88.5	44.5	482	1 BXRT	coagulation factor
10	86	43.2	416	1 KFB0	coagulation factor
11	86	43.2	617	2 S15011	thrombin (EC 3.4.2
12	86	43.2	618	2 A35827	thrombin (EC 3.4.2
13	83	41.7	461	1 KPHU	coagulation factor
14	80.5	40.5	475	1 EXCH	coagulation factor
15	78	39.2	452	1 A30351	coagulation factor
16	78	39.2	459	2 JQ0419	plasma protein Z -
17	75	37.7	396	1 KXBOZ	protein C (activat
18	73.5	36.9	461	1 IXKHU	thrombin (EC 3.4.2
19	73	36.7	622	1 TPHU	plasma protein Z P
20	70	35.2	422	1 KKHUZ	thrombin (EC 3.4.2
21	69	34.7	625	1 TBO	probable MAP kinas
22	61.5	30.9	576	2 G96763	probable MAP kinas
23	61	30.7	594	2 C96575	probable MAP kinas
24	61	30.7	603	2 S53433	plasma protein S P
25	58.5	29.4	642	2 S53433	plasma protein S P
26	56	28.1	675	1 KXROS	plasma protein S P
27	55.5	27.9	675	1 KXMSS	growth arrest-spec
28	55	27.6	673	2 A48089	protein-Tyrosine k
29	53.5	26.9	642	2 S53434	vascular endotheli

ALIGNMENTS

RESULT 1
KPHU7

Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 09-Jul-2004

C;Accession: A28322; A23819; A31186; B31186; S61524

R;O'Hara, P.J.; Grant, F.J.; Haldeman, P.J.; O'Hare, R.G.; Hart, C. Proc. Natl. Acad. Sci. U.S.A., 84, 5158-5162, 1987

A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein

A;Reference number: A28322; MUID:87260948; PMID:3037537

A;Accession: A28322

A;Molecule type: DNA

A;Residues: 1-466 <HAG>

A;Cross-references: UNIPROT:PO8709; GB:J02933; NID:9180333; PID:AAA51983; 1; PID:g180334

R;Hegen, F.S.; Gray, C.L.; O'Hare, P.J.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C. Proc. Natl. Acad. Sci. U.S.A., 83, 2412-2416, 1986

A;Title: Characterization of a cDNA coding for human factor VII.

A;Reference number: A23819; MUID:86205956; PMID:3486420

A;Accession: A23819

A;Molecule type: mRNA

A;Residues: 1-466 <HAG>

A;Cross-references: GB:MI3232; NID:g182799; PID:AAA88040; 1; PID:g182801

R;Thim, L.; Bioern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.; Biochemistry 27, 7785-7793, 1988

A;Title: Amino acid sequence and posttranslational modifications of human factor VII-a f

A;Reference number: A90539; PMID:3264725

A;Accession: A31186

A;Molecule type: protein

A;Residues: 61-212 <TH1>

A;Accession: B31186

A;Molecule type: protein

A;Residues: 213-466 <TH2>

R;Bioern, S.; Poster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen, R.; Biochem. 26, 11051-11057, 1991

J. Biol. Chem. 266, 11051-11057, 1991

A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations at A;Reference number: A40529; PMID:91259411

A;Content: annotation; carbohydrate binding sites

R;Persson, E.; Petersen, L.C.; Bur. J. Biochem. 234, 293-300, 1995

A;Title: Structurally distinct Ca(2+) binding sites in the gamma-carboxy A;Reference number: S63524; MUID:852955

A;Accession: S63524

A;Molecule type: protein

A;Residues: 61-65;99-103;105-109;213-217;308-312 <PER>

C;Genetics

A;Gene: GDB:F7

A;Cross-references: GDB:1119897; OMIM:227500

A;Map position: 13q34-13q34

A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 267/3; 269/1

C;Function:

A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor

A; Pathway: blood coagulation extrinsic pathway
 C; Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide; signal sequence #status predicted <SIG>
 F; 1-20/Domain: propeptide #status predicted <PRO>
 F; 45-104/Domain: Glia domain homology <GLA>
 F; 65-212/Domain: coagulation factor VII light chain #status experimental <MA1>
 F; 151-187/Domain: BGF homology <EGF>
 F; 223-466/Product: coagulation factor VIIA heavy chain #status experimental <MA2>
 F; 66-67-74/Domain: trypsin homology <TRY>
 F; 77-82-110-121-115-130-132-141-151-162-158-172-174-187-195-322-219-224-238-254-370-389-
 F; 112-213/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 233-302-404/Active site: His, Asp, Ser #status Predicted
 F; 350-351/Cleavage site: Arg-Gly (Coagulation factor Xa) #status predicted
 Query Match Score 81.2%; Pred. No. 2.5e-19; Length 466;
 Best Local Similarity 75.6%; Pred. No. 2.5e-19; Indels 1; Gaps 1;
 Matches 34; Conservative 0; Mismatches 10;

Qy 1 ANAYPLXXLRPGSLXRXCXQCSPEXXARXIFKDAKRTRKLFWIY 45
 Db 61 ANA-FLEELRPGSLRECKEPEQCSPEEARIFKDAERTKLFWIY 104

RESULT 2

I46332 coagulation factor VII - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C; Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
 C;Accession: I46932
 R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
 Thromb. Res. 69, 231-238, 1993
 A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
 A;Reference number: I46332; MUID:8383365
 A;Cross-references: GB:556300; NID:9266294; PID:g266295
 C;Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology
 F; 2-83/Domain: Glia domain homology <GLA>
 F; 89-120/Domain: BGF homology <EGF>
 F; 110-166/Domain: BGF homology <EGF>
 F; 192-425/Domain: trypsin homology <TRY>

Query Match Score 64.1%; Pred. No. 1.4e-13; Length 443;
 Best Local Similarity 57.8%; Pred. No. 1.4e-13;
 Matches 26; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 ANAYPLXXLRPGSLXRXCXQCSPEXXARXIFKDAKRTRKLFWIY 45
 Db 40 ANS-FLEELRPGSLRECKEPEQCSPEEARVFKQSTERIKQFWIY 83

RESULT 4

JX0210 protein C (activated) (EC 3.4.21.69) precursor - mouse
 N;Alternate names: vitamin K-dependent serine proteinase
 C;Species: Mus musculus (house mouse)
 C;Date: 10-Sep-1999 #Sequence_revision 10-Sep-1999
 C;Accession: JX0210
 Query Match Score 56.8%; Pred. No. 3.6e-11;
 Best Local Similarity 51.2%; Pred. No. 3.6e-11;
 Matches 21; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 5 FFLXLRLPSLXPXCKXQCSPEXXARXIFKDAKRTRKLFWIY 45
 Db 4 FLLBLLPGSLRECREELCSFEEBAHEIFRNNEETRQFWVSY 44

RESULT 5

JX0210 coagulation factor X; BGF homology; Gla domain homology; trypsin homology
 A;Residues: 1-461 <TD>
 A;Cross-references: UNIPROT:P31587; GB:D10445; NID:9220385; PID:BAA01235.1; PID:9220386
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that rec-
 C;Superfamily: coagulation factor X; BGF homology; Gla domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; calcium binding; carboxyglutamyl peptide; signal sequence #status predicted <SIG>
 F; 1-33/Domain: Glia domain homology <GLA>
 F; 27-85/Domain: Glia domain homology <GLA>
 F; 34-41/Domain: protein C #status predicted <PRO>
 F; 42-196/Domain: protein C #status predicted <PRC>
 F; 42-196/Domain: light chain #status predicted <CLD>
 F; 51-130/Domain: BGF homology <EG1>
 F; 139-174/Domain: BGF homology <EG2>
 F; 199-461/Domain: heavy chain #status predicted <PCH>
 F; 199-211/Domain: activation peptide #status predicted <ACT>

R; McMullen, B.A.; Fujikawa, K.; Kisiel, W. Biophys. Res. Commun. 115, 8-14, 1983
 A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor VII
 A;Reference number: A20274; MUID:83308813; PMID:6688526
 A;Accession: C20274
 A;Molecule type: protein
 A;Residues: 58-62; X, 64-68 <MCM>
 A;Note: the residue designated 'X' was determined to be hydroxyaspartic acid
 R; Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Miyata, T.; Iwanaga, S. J. Biochem. 104, 967-968, 1988
 A;Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor VII
 A;Reference number: A44556; MUID:8921399; PMID:319637
 A;Contents: annotation
 A;Note: structure and location of covalently bound carbohydrate
 C;Function:
 A;Description: catalyzes the proteolytic activation of coagulation factor X in the presence of calcium and tissue factor
 A;Pathway: blood coagulation extrinsic pathway
 C;Superfamily: coagulation factor X; BGF homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl peptide
 F; 1-152/Product: coagulation factor VII light chain #status experimental <MA1>
 F; 50-81/Domain: Glia domain homology (fragment) <GLA>
 F; 51-127/Domain: BGF homology <EG2>
 F; 153-407/Product: coagulation factor VIIA heavy chain #status experimental <MA2>
 F; 51-387/Domain: tryptophan homology <TRY>
 F; 67-1416-19, 20-25, 26, 29, 34, 35/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F; 17-22-50-61, 55-72-81-91-102, 98-112-114-127, 135-262, 159-164-178-194, 310-329, 340-348/I
 F; 52/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F; 53/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experimental
 F; 145-203/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F; 152-154/Cleavage site: Arg-Ile (coagulation factor XIA) #status experimental
 F; 193-242, 344/Active site: Arg-Gly (coagulation factor Xa) #status predicted
 F; 290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

F;212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIR>
 F;212-445/Domain: trypsin homology <TRY>
 F;47,48,55,57,60,61,66,67,70,76/Modified site: Gamma-carboxyglutamic acid (Glu) #status
 F;121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #status
 F;214-290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;253,299,402/Active site: His, Asp, Ser #status predicted

Query Match 1 ANAYFLXXLRPGSLXRXCKXXXQCSFXKARXIFKDAXRTKLFWISY 45
 Best Local Similarity 49.5%; Score 98.5%; DB 1; Length 461;
 Matches 21; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

Query Match 2 ANS-FLEEMRPSLLERCMEEICDFEEAQEIFQNVEDTLLATWKY 85
 Best Local Similarity 49.4%; Score 93.5%; DB 1; Length 456;
 Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

RESULT 5
 KXBO
 protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
 N;Alternate names: autoproteobin LIA; Plasma protein C
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text_change 09-Jul-2004
 C;Accession: A26250; Al18385; A00928
 A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
 A;Reference number: A26250; MUID:6091100
 A;Accession: A26250
 A;Molecule type: mRNA
 A;Residues: 1-156 <LON>
 A;Cross-references: UNIPROT:P00745
 R;Fernlund, P.; Stenflo, J.
 J. Biol. Chem. 257, 12170-12179, 1982
 A;Title: Amino acid sequence of the light chain of bovine protein C.
 A;Reference number: A18385; MUID:83007325; PMID:6896876
 A;Molecule type: protein
 A;Residues: 40-194 <PER>
 A;Note: B2-Lys was also found
 R;Drakenberg, T.; Fornlund, P.; Roepstorff, P.; Stenflo, J.
 Proc. Natl. Acad. Sci. U.S.A. 80, 1802-1806, 1983
 A;Title: beta-hydroxyaspartic acid in vitamin K-dependent protein C.
 A;Reference number: A19316; MUID:83169759; PMID:6572939
 A;Contents: annotation; revision to residue 110
 R;Stenflo, J.; Fernlund, P.
 J. Biol. Chem. 257, 12180-12190, 1982
 A;Title: Amino acid sequence of the heavy chain of bovine protein C.
 A;Reference number: A18386; MUID:83007326; PMID:6896877
 A;Accession: A18386
 A;Molecule type: protein
 A;Residues: 40-454, PV, <STE>
 R;Emon, N.L.; Debault, L.E.; Emon, C.T.
 J. Biol. Chem. 258, 5548-5553, 1983
 A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless F
 A;Reference number: A37511; MUID:83213513; PMID:6304092
 A;Contents: annotation; activation; calcium binding
 R;Johnson, A.E.; Emon, N.L.; Laue, T.M.; Emon, C.T.
 J. Biol. Chem. 258, 5554-5560, 1983
 A;Title: Structural changes required for activation of protein C are induced by Ca2+ bin
 A;Contents: annotation; activation; calcium binding
 C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a tetradecapeptide from the amino end of the heavy chain; this reaction is catalyzed by the thrombin-thrombomodulin complex.
 C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin B₆-dependent modification.
 C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reacts with calcium ions.
 C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is cleaved by a tetradecapeptide from the amino end of the heavy chain; this reaction is catalyzed by the thrombin-thrombomodulin complex.

F;30-39/Domain: propeptide #status predicted <PRO>
 F;40-194/Product: protein C light chain #status experimental <LCH>
 F;98-128/Domain: EGFR homology <EG1>
 F;117-172/Domain: EGFR homology <EG2>
 F;197-456/Product: protein C heavy chain #status experimental <HCH>
 F;197-210/Domain: activation peptide #status experimental <APT>
 F;211-440/Domain: trypsin homology <TR>
 F;45,46,53,55,58,59,62,64,65,68/Modified site: gamma-carboxyglutamic acid (Glu) #status
 F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental <ASP>
 F;119-128,137-148,144-157,159-172,180-318,237-253,393-431/Disulfide bonds: #status predicted
 F;136,289,350/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;255,298,397/Active site: His, Asp, Ser #status predicted
 F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1 ANAYFLXXLRPGSLXRXCKXXXQCSFXKARXIFKDAXRTKLFWISY 45
 Best Local Similarity 44.4%; Score 93.5%; DB 1; Length 456;
 Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

Query Match 2 ANS-FLEELRPGNVEREBCSEBEARIFQNTEDTNAWSFY 83
 Best Local Similarity 44.4%; Score 93.5%; DB 1; Length 456;
 Matches 20; Conservative 5; Mismatches 19; Indels 1; Gaps 1;

RESULT 6
 EXHU
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human
 N;Alternate names: Stuart factor
 C;Species: Homo sapiens (man)
 C;Date: 15-Nov-1984 #sequence revision 02-May-1994 #text_change 09-Jul-2004
 C;Accession: A24478; JQ0917; A42465; A25853; A22208; A21284; A20362; S39415; I54051; A00:
 R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
 Biochemistry 25, 5098-5102, 1986
 A;Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e
 A;Reference number: A24478; PMID:3768336
 A;Accession: A24478
 A;Molecule type: DNA
 A;Residues: 1-488 <LEY>
 A;Cross-references: UNIPROT:P00742; GB:L299433; GB:MI1327; NID:9459809; PIDN:AA552764.1; I
 R;Messier, T.J.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
 Gene 99, 291-294, 1991
 A;Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag
 A;Reference number: JQ0917; PMID:91216473; PMID:1902434
 A;Accession: JQ0917
 A;Molecule type: mRNA
 A;Residues: 1-488 <MES>
 A;Cross-references: GB:MS7285; NID:912389; PIDN:AA52421.1; PID:gi182390
 R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
 J. Biol. Chem. 267, 7395-7401, 1992
 A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagulate
 A;Reference number: A42485; MUID:92218390; PMID:1313796
 A;Accession: A42485
 A;Molecule type: DNA
 A;Residues: 1-15 <MAA>
 A;Experimental source: liver
 A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIPI:93787)
 R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
 Gene 41, 311-314, 1996
 A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
 A;Reference number: A25853; MUID:862221713; PMID:3011603
 A;Accession: A25853
 A;Molecule type: mRNA
 A;Residues: 19-284, 'E', 289-488 <KAU>
 A;Cross-references: GB:M22613; NID:gi180335; PIDN:AA51984.1; PID:gi180336
 R;Fung, M.; Macmillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985
 A;Title: Characterization of an almost full-length cDNA coding for human blood coagulatic
 A;Reference number: A22208
 A;Accession: A22208
 A;Molecule type: mRNA
 A;Residues: 13-441, 'S', 443-488 <FUN>
 A;Cross-references: GB:K03194; NID:gi182840; PIDN:AA52490.1; PID:gi182841
 R;Leytus, S.P.; Chung, D.W.; Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A;Title: Characterization of a cDNA coding for human factor X.
A;Accession: A21284; MUID:84222026; PMID:6587384
A;Molecule type: mRNA
A;Residues: 13-284; E; 289-488 <L82>
A;Cross-references: GB:K01886
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weine Biochemistry 22, 2875-2884, 1983
A;Title: Complete amino acid sequence of the light chain of human blood coagulation factor X.
A;Reference number: A20362; MUID:83257207; PMID:6871167
A;Accession: A20362
A;Molecule type: protein
A;Residues: 41-175 <MCMs>
A;Inquire, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993
A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A;Reference number: S3914; MUID:94062825; PMID:8243461
A;Accession: S39415
A;Molecule type: protein
A;Residues: 183-234 <INO>
A;Note: Glycosylation sites
A;Note: Identification and characterization of beta-hydroxyaspartic acid
R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hansabhuhanam, R.; Lyman, G.
Gene 84, 517-519, 1989
A;Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A;Reference number: 154051; MUID:90128299; PMID:2612918
A;Accession: 154051
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:M33297; NID:gi183860; PIDN:AAA52636_1; PMID:g553330
R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Huber, R.; Bla J. Mol. Biol. 232, 947-956, 1993
A;Title: Structure of human des(1-45) Factor Xa at 2.2 angstroms resolution.
A;Reference number: A4958; MUID:9360277; PMID:8355279
A;Contents: annotation; X-ray crystallography, 2.2 angstroms
C;Comment: The two chains held together by one disulfide bond are formed from a single-chain; Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
C;Genetics:
A;Gene: GDB:F00
A;Cross-references: GDB:119890; OMIM:227600
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam P;1/23/Domain: signal sequence #status predicted <SIG>
P;2/40/Domain: propeptide #status predicted <PRO>
F;2/84/Domain: Gla domain homology <GHA>
F;4/179/Product: coagulation factor X light chain #status experimental <LCH>
F;9/1-121/Domain: EGF homology <EGI>
F;129-164/Domain: EGF homology <EG2>
F;183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
F;183-234/Domain: activation Peptide #status experimental <APT>
F;225-462/Domain: trypsin homology <TRY>
F;5/5-62/Disulfide bonds: #status Predicted
F;9/101-95/110/112-121/129-140/136-149/151-164/172-342/241-246/261-277/390-404/415-443/ F;113/Modified site: erythro-beta-hydroxyaspartic acid (asp) #status experimental
F;119/211/Domain: activation Peptide #status Predicted
F;21/23/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;24/235/Cleavage site: carbohydrate (Asn) (covalent) #status experimental Factor VIIA) #statat F;216, 322-419/Active site: His, Asp, Ser #status experimental
Query Match Score 91.5; DB 1; Length 488;
Best Local Similarity 40.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 8; Mismatches 18;
Indels 1; Gaps 1;
Qy 1 ANAYFLXXLRPGSLXRXCXXQCSFXXARXIFKDAXRTKLFWISY 45

Db 41 ANS-FLEEMKGHLERMEETCSYEAREREVFDSDDKTNEFWNKY 84

RESULT 7

EXJO

coagulation factor Xa (EC 3.4.21.6) precursor - bovine

N;Alternative names: Stuart factor

C;Species: Bos primigenius taurinus (cattle)

C;Date: 24-Apr-1984 #sequence revision 117-Mar-1987 #text change 09-Jul-2004

C;Accession: A22867; A1499; A12030; A34112; S39414; A00525

R;Pung, M.R.; Campbell, R.M.; MacGillivray, T.A.

Nucleic Acids Res. 12, 4481-4492, 1984

A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A;Reference number: A22867; MUID:84227315; PMID:6310671

A;Accession: A22867

A;Molecule type: mRNA

A;Residues: 1-487 <ENF>

R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood clotting factor Xa

A;Reference number: A20274; MUID:833208813; PMID:6688526

A;Contents: annotation; revision to residue 103
R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975

A;Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A;Reference number: A14997; MUID:80130563; PMID:6766753

A;Accession: A14997

A;Molecule type: protein
A;Residues: 41-102, N, 104-180 <ENF>

R;Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989

A;Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal ζ -peptides
A;Reference number: A12030; PMID:76053069; PMID:1039093

A;Accession: A12030

A;Molecule type: protein
A;Residues: 183-292/224-295, 'GDE', 299-334-336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <T>
A;Note: carbohydrate binding sites and disulfide bonds were determined
A;Note: beta-hydroxyaspartic acid site

R;Inoue, K.; Morita, T.
Eur. J. Biochem. 218, 153-163, 1993

A;Title: Identification of O-linked oligosaccharide chains in the activation peptides of
A;Reference number: S39414; MUID:823461; PMID:2789221

A;Accession: A33412

A;Molecule type: protein
A;Residues: 85-126 <PRP>

A;Note: beta-hydroxyaspartic acid site

R;Titani, K.; Hermansson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; Davies, B.W.
Biochemistry 11, 4899-4903, 1972

A;Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian
A;Reference number: A12453; MUID:73053314; PMID:4234286

A;Contents: annotation; active site
R;Fujikawa, K.; Titani, K.; Davies, B.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975

A;Title: Activation of bovine factor X (Stuart factor); conversion of factor Xalpha to I
A;Contents: annotation; active site
R;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, S705-S710, 1984

A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A;Reference number: A38024; PMID:6569300

A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986

A;Reference number: A38025; MUID:86140210; PMID:3949800

A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of two activation peptide. The activation peptide is cleaved by factor IXa (in the intrinsic pathway).
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong affinity, activates Factor Xa. The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C-Genetics:
A;Gene: F10
A;Map position: 13q34
C;Function:
A;Pathway: blood coagulation
C;Superfamily: coagulation factor X; EGFP homology; Gla domain homology; trypsin homology
C;Keywords: bera-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamate; signal sequence
A;1-15/Domain: signal sequence #status predicted <SIG>
A;F/F: 16-40/Domain: propeptide #status predicted <PRO>
A;F/F: 25-84/Domain: Gla domain homology <Gla>
A;F/F: 41-180/Product: coagulation factor X light chain #status experimental <LCX>
A;F/F: 90-121/Domain: EGFP homology <EG1>
A;F/F: 129-164/Domain: EGFP homology <EG2>
A;F/F: 183-492/Product: coagulation factor X heavy chain #status experimental <HC>
A;F/F: 234-492/Product: coagulation factor X heavy chain #status experimental <HNC>
A;F/F: 234-461/Domain: trypsin homology <TRY>
A;F/F: 46-47, 56-59, 60-65, 66-69, 72-75, 79/Modified site: Gamma-carboxyglutamic acid (Glu) #status experimental <Gla>
A;F/F: 57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-341/Disulfide bonds: #status experimental <PRO>
A;F/F: 103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
A;F/F: 200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
A;F/F: 208/Binding site: carbohydrate (Asn) (covalent) #status experimental
A;F/F: 218/Binding site: carbohydrate (Asn) (covalent) #status experimental
A;F/F: 233-234/Cleavage site: Arg-Lys (coagulation factor IXa, coagulation factor VIIa) #status experimental
A;F/F: 240-245, 389-403, 414-442/Disulfide bonds: #status experimental
A;F/F: 275, 321, 418/Active site: His, Asp, Ser #status predicted
Query Match 45.5%; Score 90.5%; DB:1; Length 492;
Best Local Similarity 42.2%; Pred. No. 2.8e-01;
Matches 19; Conservative 7; Mismatches 18; Indels 1; Gaps 1;
C;Accession: S18994; S24312 _sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Description: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994
A;Accession: S18994
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OXA>
A;Cross-references: UNIPROT:P11394; EMBL:X64316; NID:956962; PIDN:CAA45617.1; PID:956963
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
C;Submitted to the EMBL Data Library; February 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S18994
A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OXA>
A;Cross-references: EMBL:X64316; NID:956962; PIDN:CAA45617.1; PID:956963
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
C;Submitted to the EMBL Data Library; February 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312
A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OXA>
A;Cross-references: EMBL:X64316; NID:956962; PIDN:CAA45617.1; PID:956963
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
C;Submitted to the EMBL Data Library; February 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312
A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OXA>
A;Cross-references: EMBL:X64316; NID:956962; PIDN:CAA45617.1; PID:956963
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S18994; S24312
C;Submitted to the EMBL Data Library; February 1992
A;Title: The cDNA cloning and mRNA expression of rat protein C.
A;Reference number: S24312
A;Accession: S24312
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <OXA>

F:/129-16-/Domain: BGF homology <EG2>	
F:/183-231-/Domain: coagulation factor X heavy chain #status predicted <HCH>	
F:/183-231-/Product: activation peptide #status predicted <APT>	
F:/332-482-/Domain: coagulation factor Xa heavy chain #status predicted <ACT>	
F:/332-482-/Product: trypsin homology <TRY>	
F:/F:16-47-54:56-59:60-65:66-69:72-79/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <GAG>	
F:/F:51-62:90-101:95-110:112-121:129-140:156-157:164:172-340:238-243:259-275:388-402:41	
F:/F:103-/Modified site: erythro-hydroxyaspartic acid (Asp) #status predicted <ASP>	
F:/F:187-/Modified site: carbohydrate (Asn) (covalent) #status experimental <CAR>	
F:/F:208-/Binding site: carbohydrate (Thr) (covalent) #status predicted <THR>	
F:/F:218-/Binding site: carbohydrate (Asn) (covalent) #status predicted <ASN>	
F:/F:231-232/Cleavage site: Arg(ile) (coagulation factor IXa, coagulation factor VIIa) #status predicted <STAT>	
Query Match 44.5% Score 88.5: DB 1; Length 482;	
Best Local Similarity 40.0%; Pred. No. 5.9e-07;	
Matches 18; Conservative 8; Mismatches 18; Indels 1; Gaps 1;	
Qy 1 ANAYFXXLRLPQGSILRXCXQXQCSPXXARXKIFDKDARTKLFWISY 45	
Db 41 ANSFPFEEIKKGNLREECVBICSPFBEAREVFEDNEKTTPEWNKY 84	
RESULT 10	
KFB0	
coagulation factor IXa (BC 3.4.21.22) precursor - bovine	
N/Alternative names: Christmas factor	
C/Species: Bos primigenius tauris (cattle)	
C/Accession: A147591; B20274; I45891; A09023	
R/R/Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti	
Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979	
A/Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa	
A/Reference number: A14757; PMID:80056619; PMID:231916	
A/Molecule type: protein	
A/Residues: 1-63 'T', 65-416 <KAT>	
R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.	
Biochem. Biophys. Res. Commun. 115, 8-14, 1983	
A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factor IXa	
A/Accession: B20274	
A/Molecule type: protein	
A/Residues: 59-63 'X', 65-69 <MCMD>	
R/Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.	
Nature 299, 178-180, 1992	
A/Title: Molecular cloning of the gene for human anti-haemophilic factor IX.	
A/Reference number: A145891; PMID:83308883; PMID:688526	
A/Accession: I45891	
A/Content: translated from GB/EMBL/DDJB	
A/Molecule type: protein	
A/Residues: 52-139 <CHO>	
A/Cross-references: GB:200007; NID:9163053; PID:AAA30520.1; PMID:g163054	
R/Hase, S.; Kawamura, S.; Niishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,	
J. Biochem. 104, 867-868, 1988	
A/Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factor IXa	
A/Content: annotation	
A/Note: structure and location of a carbohydrate covalently bound to Ser	
C/Comment: Factor IX is activated by factor Xa, which excises the activation peptide propeptide from the gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-dependent modification. Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stroma, activates the proteolytic activation of coagulation factor X in the presence of a carbonyl group.	
C/Products: coagulation factor X; EGII homology; Gla domain homology; trypsin homology	
C/Peptides: superfamily; coagulation factor X; EGII homology; Gla domain homology; trypsin homology	
C/Peptides: superfamily; coagulation factor X; EGII homology; Gla domain homology; trypsin homology	
F:/1-16-/Product: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamyl	
F:/1-45-/Product: coagulation factor IXa light chain #status experimental <ALC>	
C/Function:	
A/Description: catalyzes the proteolytic activation of coagulation factor X in the presence of a carbonyl group.	
A/Pathway: blood coagulation intrinsic pathway	
C/Peptides: superfamily; coagulation factor X; EGII homology; Gla domain homology; trypsin homology	
C/Peptides: superfamily; coagulation factor X; EGII homology; Gla domain homology; trypsin homology	
F:/51-82/Domain: EGII homology <EGII>	
F:/88-124/Domain: EGII homology <EGII>	
F:/147-181/Domain: activation peptide #status experimental <APT>	

thrombin (EC 3.4.21.5) precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 09-Jul-2004
 C;Accession: A35827; A422696; S12081
 R;Degen, S.J.F.; Schaefer, L.A.; Janison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
 DNA Cell Biol. 9, 487-498, 1990
 A;Title: Characterization of the cDNA coding for mouse prothrombin and localization of b
 A;Reference number: A35827; MUID:91025551; PMID:2222810
 A;Accession: A35827
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-618 <DB>
 A;Cross-references: UNIPROT:P19221; GB:X52308; PID:953813; PID:CAA36548.1; PID:953814
 A;Experimental source: strain C57BL/6
 A;Note: the data were obtained from females resulting from the cross of M. domesticus and R;Banfield, D.K.; MacGillivray, R.T.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing
 A;Reference number: A42696; MUID:92212913; PMID:1557383
 A;Accession: A42696
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 384-618, 'E', <BAN>
 A;Cross-references: GB:MB1394
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
 C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydrophobicity; signal sequence; status predicted <SIG>, F1-24/Domain: signal sequence; status predicted <SIG>, F1-24/Domain: signal sequence; status predicted <PRO>, F28-88/Domain: propeptide #status predicted <PRO>, F44-618/Product: prothrombin B #status predicted <MAT>, F109-187/Domain: kringle homology <KR1>, F125-293/Domain: kringle homology <KR2>, F361-610/Domain: trypsin homology <TRY>, F501-56, 91-104, 109-187, 130-170, 182, 215-293, 236-276, 288, 333-479, 388-404, 533-547, 5 F403, 459, 565/Active site: His, Asp, Ser #status predicted
 Query Match Score 86; DB 2; Length 618;
 Best Local Similarity 40.0%; Pred. No. 2e-06;
 Matches 18; Conservative 5; Mismatches 22; Indels 0; Gaps 0;
 Qy 1 ANAYFLXXLRPGSLXRXCKQXQCSFXKARXKFKDAXRKTFLWISY 45
 Db 44 ANSGPFLERLKGNLNEREVCSEOCSEAEFALESPQDTDFWAKY 88

RESULT 13
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A00922; A37570; A30511; A32989; A22673; A37337; A37546; A30623; A60486; A20
 R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3726-3730, 1985
 A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A;Reference number: A00922; MUID:8600558; PMID:2994716
 A;Accession: A00922
 A;Molecule type: DNA
 A;Residues: 1-161 <YOS>
 A;Cross-references: UNIPROT:P00740; GB:K02402; NID:9102612; PID:9182613
 R;Aanson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddleston, J.A.; Bro
 EMBO J. 3, 1053-1060, 1984
 A;Title: The gene structure of human anti-haemophilic factor IX.
 A;Reference number: A37570; MUID:84236100; PMID:6329734

KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Dec-1982 #sequence 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A00922; A37570; A30511; A32989; A22673; A37337; A37546; A30623; A60486; A20
 R;Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3726-3730, 1985
 A;Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A;Reference number: A00922; MUID:8600558; PMID:2994716
 A;Accession: A00922
 A;Molecule type: DNA
 A;Residues: 1-161 <ANS>
 A;Cross-references: GB:K02048
 R;Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemsma, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A;Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A;Reference number: A30511; MUID:88327116; PMID:3416069

A; Molecule type: mRNA; protein
 A; Residues: 1-68 <JAL>
 A; Note: processed forms expressed in recombinant system
 R; Hafford, P.A.; Baron, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell, R.; Haemost. J., 9, 475-480, 1990
 A; Title: The first EGF-like domain from human factor IX contains a high-affinity calcium binding site
 A; Reference number: S12377; MUID:90151623; PMID:2406129
 A; Accession: S12377
 A; Molecule type: protein
 A; Residues: 92-130 <HANS>
 A; Note: NMR detection of calcium binding by domain expressed in recombinant system
 R; De la Salle, C.; Charmantier, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993
 A; Title: A deletion located in the 3' non translated part of the factor IX gene responsible for the absence of factor IXa in patients with hemophilia B
 A; Reference number: I59612; MUID:9405330; PMID:823650
 A; Accession: I59612
 A; Status: translatable from GB/EMBL/DBBJ
 A; Molecule type: DNA
 A; Residues: 44-461 <RES>
 A; Cross-references: GB:66752; PIDN:AAB28588.1; PID:94399774
 R; Soflet, E.S.; Koerber, D.D.; Sarkar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A; Title: Genomic amplification with transcript sequencing.
 A; Reference number: I59229; MUID:88127096; PMID:3340835
 A; Accession: I59229
 A; Status: translatable from GB/EMBL/DBBJ
 A; Molecule type: DNA
 A; Residues: 290-359 <RES>
 A; Cross-references: GB:119062; PIDN:q182622; PID:9182623
 R; Asarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iwahashi, T.; Biochemistry 33, 5167-5171, 1994
 A; Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically linked to carbohydrazide side chains
 A; Reference number: A54255; MUID:942207047; PMID:817892
 A; Accession: A54255
 A; Molecule type: protein
 A; Residues: 'D', 'P04', 'X', '206-211', '212', 'D', '214', 'X', '216-221', 'D', <AGA>
 A; Note: the residues designated 'X' were determined to be threonine bound to carbohydrazide side chains
 R; Di Scipio, R.G.; Kurachi, K.; Davies, B.W.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984
 J. Clin. Invest. 61, 1528-1538, 1978
 A; Content: Activation of human factor IX (Christmas Factor).
 A; Reference number: A18843; MUID:7819509; PMID:659613
 A; Contents: annotation; activation; active site; carbohydrate binding
 R; McGrath, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984
 A; Content: annotation; active site; carbohydrate binding
 R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A; Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding site
 A; Reference number: A37543; MUID:64185715; PMID:6425596
 A; Content: annotation; calcium binding
 R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583-2585, 1985
 A; Content: annotation; calcium binding, correction
 R; Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A; Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A; Reference number: A37545; MUID:8618947; PMID:3009023
 A; Content: annotation; signal sequence cleavage site
 R; Seehiro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J. Biol. Chem. 264, 21257-21265, 1989
 A; Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
 A; Reference number: A30622; MUID:90078229; PMID:2592373
 A; Content: annotation; sequence of mutant B(M) Nagoya
 R; Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee submitted to the Brookhaven Protein Data Bank, November 1991
 A; Content: annotation; conformation by (1)H-NMR, residues 92-130
 A; Note: recombinant form expressed in yeast
 C; Comment: Factor IX is activated by factor XIA, which excises the activation peptide prior to the thrombin cleavage site.

C; Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-dependent modification of the protein. Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strong genetic evidence, it is clear that the Gla residues are the targets of the posttranslational modification.
 C; Function: Catalyzes the proteolytic activation of coagulation factor X in the presence of thrombin. Haemost. J., 70, 370-371, 1993
 A; Function: Catalyzes the proteolytic activation of coagulation factor X in the present A; Pathway: blood coagulation intrinsic pathway
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid; signal sequence
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:1-29-46/Domain: Propeptide #status experimental <PPR>
 F:1-91/Domain: Gla domain homology
 F:1-91-91/Domain: Gla domain homology <GLA>
 F:1-191/Domain: coagulation Factor IXa light chain #status experimental
 F:1-170/Domain: EGF homology <EG1>
 F:1-192-226/Domain: activation peptide #status experimental
 F:1-227-454/Domain: coagulation Factor IXa heavy chain #status experimental <ACT>
 F:1-227-454/Domain: thrombin homology <TRY>
 F:1-53, 54, 61-63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:1-54-69, 97-108, 102-117, 119-128, 134-145, 141-157, 170-171, 195-196, 252-268, 382-396, 407-435/D
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation Factor XIa) #status experimental
 F:203, 213/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:205, 215/Binding site: Arg-Val (coagulation Factor XIa) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation Factor XIa) #status experimental
 Query Match 41-78; Score 83; DB 1; Length 461;
 Best Local Similarity 44.1%; Pred. No. 4.9e-06;
 Matches 5; Mismatches 14; Indels 0; Gaps 0;
 Qy 1.2 GSLXRXCXXXQCSFXXKXKFDAXRPLKFWSY 45
 Db 58 GNLERECMEKKCSPEEAREVFTTERTEFWKQY 91
 RESULT 14
 EXCH
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken
 N; Alternative names: virus-activating proteinase
 C; Species: Gallus gallus (chicken)
 C; Accession: S15838; S20380; S20381
 C; Date: 12-Feb-1993 #sequence revision 07-Feb-1997
 R; Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogawara, T.; Nakamura, T.; Yamuchi, F.; Ogawara, T.; Nagai, Y.
 FEBS Lett. 283, 281-285, 1991
 A; Title: Primary structure of the virus activating protease from chick embryo. Its identity with the virus activating protease from chicken embryo
 A; Reference number: S15838; MUID:91257322; PMID:2044767
 A; Accession: S15838
 A; Status: not compared with conceptual translation
 A; Molecule type: mRNA
 A; Residues: 1-475 <SU2>
 A; Cross-references: UNIPROT: P25155; DDBJ: D00844; NID: g222869; PIDN: BAA00724.1; PID: g22287;
 R; Gotoh, B.; Yamuchi, F.; Ogawara, T.; Nagai, Y.
 FEBS Lett. 296, 274-278, 1992
 A; Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible for the amniotic membrane
 A; Reference number: S20380; MUID: 92164779; PMID: 15317403
 A; Accession: S20380
 A; Molecule type: protein
 A; Residues: 41-45 <G02>
 A; Accession: S20381
 A; Molecule type: protein
 A; Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
 C; Function: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of thrombin
 A; Pathway: blood coagulation
 C; Superfamily: coagulation Factor X; EGF homology
 C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic acid; signal sequence #status predicted <SIG>
 F:1-20/Domain: signal sequence #status predicted <PRO>
 F:21-40/Domain: Propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>

F;41-185/Product: coagulation factor X light chain #status experimental <LCH>
 F;90-121/Domain: EGF homology <EG1>
 F;129-167/Domain: EGF homology <EG2>
 F;186-240/Domain: activation peptide #status predicted <APT>
 F;241-475/Product: coagulation factor X heavy chain #status predicted <HCH>
 F;241-468/Domain: trypsin homology <TRY>
 F;46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #
 F;57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,241-252,267-283,396-410,42
 F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F;196-207,228-285/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;282,328-425/Active site: His, Asp, Ser #status predicted

Query Match Score 40.5%; Score 80.5%; DB 1; Length 475;
 Best Local Similarity 37.8%; Pred. No. 1.3e-05;
 Matches 17; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy	1 ANAYFLXXLRPSSLXRXCKXXXQCSFXKARXPKDADRTKLFWIY 45
Db	41 ANS-FLEEMKGQNIERECNECRCSKEEARAEFDNEKTEFWIY 84

RESULT 15

A30351 coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A30351; I46201
 R;Evans, J.P.; Watzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1989
 A;Title: Molecular cloning of a cDNA encoding canine factor IX.
 A;Reference number: A30351; MUID:83323338; PMID:2752110
 A;Accession: A30351
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-452 <EVA>
 A;Cross-references: UNIPROT:PI19540; GB:N21757; NID:992719; PID:AAA75006_1; PID:g163948
 R;Axelrod, J.H.; Read, M.S.; Brinkhous, K.M.; Verma, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A;Keywords: phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic
 A;Reference number: I46201; MUID:90311364; PMID:2367529
 A;Accession: I46201
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-452 <EVA>
 A;Cross-references: GB:M3826; NID:9163949; PID:AAA30844_1; PID:g163950
 C;Superfamily: coagulation factor X; EGF homology; Glu domain homology; trypsin homology
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-40/Domain: propeptide #status predicted <PRO>
 F;24-84/Domain: Glu domain homology <GLU>
 F;90-121/Domain: EGF homology <EG1>
 F;122-163/Domain: EGF homology <EG2>
 F;218-445/Domain: trypsin homology <TRY>
 F;46-47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #
 F;57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Di
 F;255,306-402/Active site: His, Asp, Ser #status predicted

Query Match Score 39.2%; Score 78; DB 1; Length 452;
 Best Local Similarity 41.2%; Pred. No. 3.4e-05;
 Matches 14; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy	12 GSLXRICKXQCSFXKARXPKDADRTKLFWIY 45
Db	51 GNLERECIEKCSPEEARVFENTEKTEFWIY 84

This Page Blank (uspto)

Scoring table:	BLOSUM62						ALIGNMENTS
Scorers:	Gapop 10.0 , Gapext 0.5						
Searched:	1612378 seqs, 512079187 residues						
Total number of hits satisfying chosen parameters:	1612378						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
Listing first 45 summaries							
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES	*						
Result No.	Query	Match Length	DB ID	Description			
--	--	--	--	--			
1	FA7_HUMAN	466	1	P08709 homo sapien			
2	FA7_HUMAN	81.2	679	Q96P08 homo sapien			
3	FA7_HUMAN	64.1	444	P08708 oryctolagus			
4	FA7_HUMAN	58.5	446	P08707 mus musculus			
5	FA7_BOVIN	56.8	407	P22437 bos taurus			
6	FA7_HUMAN	54.8	443	Q8jh99 brachydanio			
7	FA7_HUMAN	52.0	459	Q9gj02 sus scrofa			
8	FA7_HUMAN	49.5	460	P33597 mus musculus			
9	FA7_HUMAN	48.2	179	Q8taS3 homo sapien			
10	FA7_HUMAN	48.2	198	Q8r112 mus musculus			
11	FA7_HUMAN	48.2	202	Q9MG22 mouse			
12	FA7_HUMAN	47.7	216	Q9DfH4 xenopus tro			
13	FA7_HUMAN	47.2	442	Q804X1 fugu rubripinnis			
14	FA7_HUMAN	47.0	425	Q804X7 gallus gallus			
15	FA7_RAT	47.0	446	Q8kq6 rattus norvegicus			
16	FA7_BOVIN	45.5	1	Q6gp17 xenopus laevis			
17	FA7_BOVIN	46.2	208	Q9GP17 fugu rubripinnis			
18	FA7_BOVIN	46.2	537	Q9O4W8 fugu rubripinnis			
19	FA7_HUMAN	46.0	218	Q9M1H4 homo sapiens			
20	FA7_HUMAN	46.0	266	Q9NEK6 homo sapiens			
21	FA7_HUMAN	46.0	488	P00742 homo sapiens			
22	FA7_BOVIN	45.5	492	P00743 bos taurus			
23	FA7_BOVIN	45.0	461	P07C_RAT			
24	FA7_BOVIN	45.0	461	Q8BFY8 fugu rubripinnis			
25	FA7_BOVIN	44.5	433	Q804X5 gallus gallus			
26	FA7_HUMAN	44.5	469	Q9gm09 ornithorhynchus anatinus			
27	FA7_RAT	44.5	482	P010 RAT			
28	FA7_BOVIN	44.2	471	Q804X6 gallus gallus			
29	FA7_RABBIT	44.0	490	Q9b2G5 oryctolagus cuniculus			
30	FA7_HUMAN	43.7	226	Q9M4H6 homo sapiens			
31	FA7_HUMAN	43.5	340	Q80Y26 mus musculus			

- RT coagulation Factor VII. ";

RL Hum. Mol. Genet. 2:1355-1359 (1993).

[6] RN STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=251120;
RA Nishimura H., Kawabata S., Kistel W., Hase S., Ikenaka T., Takao T.,
RA Shimanishi Y., Iwanaga S., Nishimura H., Kawabata S., Ikenaka T.,
RA "Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyly-Glc)
RA O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human Factors VII and IX and
RT protein Z and bovine protein Z.";
RL J. Biol. Chem. 264:20320-20325 (1989).
RN [7] RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91294709; PubMed=21229367;
RA Iwanaga S., Nishimura H., Kawabata S., Ikenaka T., Hase S., Ikenaka T.,
RA "A new triaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RL Adv. Exp. Med. Biol. 281:121-131(1990).

[8] RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903; DOI=10.1038/jmbi.1998.2452;
RA Banner D.W., D'Arcy A., Chane C., Winkler F.K., Guha A.,
RA Konigshberg W.H., Nemeson Y., Kirchhofer D.;
RA "The crystal structure of the complex of blood coagulation factor VIIA
RT with soluble tissue factor.";
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 265:2089-2104 (1996).
RN [9] RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=99126538; PubMed=9325787; DOI=10.1006/jmbi.1998.2452;
RA Zhang B., St Charles R., Tulinsky A.,
RA "Structure of extracellular tissue factor complexed with factor VIIA
RT inhibited with a BPTI mutant.";
RL J. Mol. Biol. 265:41-46 (1996).
RN [10] RP STRUCTURE BY NMR OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=98367502; PubMed=9692950; DOI=10.1021/bi980522f;
RA Muranyi A., Finn B.E., Gippert G.P., Forben S., Stenflo J.,
RA Drakenberg T.;
RA "Solvation structure of the N-terminal EGF-like domain from human
RT factor VII.";
RT Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RT Blood 78:132-140 (1991).
RN [11] RP VARIANT GLN-145.
RX MEDLINE=9130046; PubMed=2070047;
RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
RA Meade T.W., Tuddenham E.G.D.;
RA "Purification and characterization of factor VII 304-Gln: a variant
RT molecule with reduced activity isolated from a clinically unaffected
RT male.";
RT Blood 78:132-140 (1991).
RN [12] RP VARIANT GLN-364 AND PHE-370.
RX MEDLINE=92340074; PubMed=1634227;
RA Marchetti G., Patrachini P., Gemmatti D., Derosa V., Pinotti M.,
RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;
RA "Detection of two missense mutations and characterization of a repeat
RT polymorphism in the factor VII gene (F7)." ;
RT Hum. Mol. Genet. 2:1055-1056 (1993).
RN [13] RP VARIANT TYR-238.
RX MEDLINE=94061028; PubMed=8242057;
RA Marchetti G., Ferrati M., Patrachini P., Redaelli R., Bernardi F.,
RA von Felten A., Neill E., Hahn T., Prangnell D.R., Lumley H.,
RA Denduham B.G.D., McVey J.H.;
RA "Detection of missense mutations by single-strand conformational
RT polymorphism (SSCP) analysis in five dysfunctional variants of
RT factor VII gene.";

[14] RN [15] RP VARIANT SER-367.
RX PubMed=7860081;
RA Devald G., Noethen M.M., Ruther K.;
RT "A common Ser/Thr polymorphism in the perforin-homologous region of
human complement component C7.";
RL Hum. Hered. 44:301-304 (1994).
RN [16] RP VARIANT VAL-354.
RX MEDLINE=95072589; PubMed=7901691;
RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
RA Rodeghiero F., Marchetti G.;
RA "Topologically equivalent mutations causing dysfunctional coagulation
RT factors VII (294Ala>Val) and X (334Ser>Pro)." ;
RT factors VII (294Ala>Val) and X (334Ser>Pro).";
RL Hum. Mol. Genet. 3:1175-1177 (1994).
RN [17] RP VARIANT MET HIS-307.
RX MEDLINE=950564662; PubMed=7974346;
RA Ohira M., Hayashi T., Wada H., Minamikawa K., Shirakawa S., Suzuki K.;
RA "Factor VIIa: homologous asymptomatic type I deficiency caused by
RT an amino acid substitution of His (CAC) for Arg (GAG) in the
catalytic domain.";
RT Thromb. Haemost. 71:773-777 (1994).
RN [18] RP VARIANT MET-419.
RX MEDLINE=96247510; PubMed=8652821;
RA Arbib A.A., Mannucci P.M., Bauer K.A.,
RA "Factor VIIa: homozygous asymptomatic type I deficiency caused by
RT defective secretion of the molecule.";
RT Blood 87:5085-5094 (1996).
RN [19] RP VARIANT TRP-283; IYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA Bernardi F./SIC10:98-1004(1996);8-2>108: AID-HUM02>3:3.CO;2-6;
RA "A Thr359Met mutation in factor VII of a patient with a hereditary
RT deficiency causes defective secretion of the molecule.";
RT Blood 87:5085-5094 (1996).
RN [20] RP VARIANT TRP-283; IYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
RX MEDLINE=97001216; PubMed=8844208;
RA Bernardi F., Casarani G., Pinotti M., Ferraresi P., di Iasio M.G.,
RA Lunghi B., Rodeghiero F., Marchetti G.;
RA "Ala244Val is a common, probably ancient mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RT Thromb. Haemost. 76:283-291 (1996).
RN [21] RP VARIANT VAL-104.
RX MEDLINE=97037613; PubMed=8803260;
RA Tamary H., Promovich L., Shalom L., Reich Z., Dym O., Lanir N.,
RA Brenner B., Paz M., Juider A.S., Blau O., Korostishevsky M., Zaitov R.,
RA Seligsohn U.;
RA "Factor VII Morioka (FVII L-22P): a homozygous missense mutation causing factor VII
RT deficiency in Moroccan and Iranian Jews.";
RT Thromb. Haemost. 76:283-291 (1996).
RN [22] RP VARIANT MORIOKA PRO-13.
RX MEDLINE=98235713; PubMed=9576180;
RA Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
RA Sakuragawa N.;
RA "Factor VII Morioka (FVII L-22P): a homozygous missense mutation in
RT the signal sequence identified in a patient with factor VII
RT deficiency.";
RT Br. J. Haematol. 101:47-49 (1998).
RN [23] RP VARIANT MALTA THR-194 AND VAL-304.
RX MEDLINE=9112461; PubMed=942082;
RA Alehino C., Scerri C., Gaidies R., Aquilina A., Felice A.B.,
RA "Two new missense mutations (P134T and A224V) in the coagulation
RT factor VII gene.";

RL	Hum. Mutat. Suppl. 1:S189-S191(1998). [24]	Query Match 81.2%; Score 161.5; DB 1; Length 466; Best Local Similarity 75.6%; Pred. No. 8.5e-20; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;	Query Match 81.2%; Score 161.5; DB 2; Length 679; Best Local Similarity 75.6%; Pred. No. 1.2e-19; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy	1 ANAYFLXXLRPGSLXRXCKXXCSFXARXARFKDAXRTKLFWIY 45	Qy 1 ANAYFLXXLRPGSLXRXCKXXCSFXARXARFKDAXRTKLFWIY 45 Db 39 ANA-PLEELRPGSLERECKEBQCSFEAREBKDAERTKLFWIY 82	Qy 1 ANAYFLXXLRPGSLXRXCKXXCSFXARXARFKDAXRTKLFWIY 45 Db 39 ANA-PLEELRPGSLERECKEBQCSFEAREBKDAERTKLFWIY 82
RESULT 2	FA7_RABBIT	PRT; 444 AA.	PRT; 444 AA.
Q96PQ8	PRELIMINARY;	PRT; 679 AA.	PRT; 679 AA.
AC	Q96PQ8_0001 (I-EMBLrel. 19, Created)	AC P98139; P79224; STANDARD;	AC P98139; P79224; STANDARD;
DT	01-DEC-2001 (I-EMBLrel. 19, Last sequence update)	DT 01-FEB-1996 (Rel. 33, Created)	DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT	01-JUN-2003 (I-EMBLrel. 24, Last annotation update)	DT 25-OCT-2004 (Rel. 45, Last annotation update)	DT Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
DE	Factor VII active site mutant immunocognjugate.	DB Name=F7;	DB Name=F7;
OS	Homo sapiens (Human).	OS Oryctolagus cuniculus (Rabbit).	OS Oryctolagus cuniculus (Rabbit).
OC	Metazoa; Chordata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.	OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
NCBI_TaxID	9606;	NCBI_TaxID=9986;	NCBI_TaxID=9986;
RN	[1]	RN [1]	RN [1]
RP	SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RX	MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;	RX TISSUE=Liver;	RX TISSUE=Liver;
RA	"Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostate cancer.";	RA MEDLINE=3190306; PubMed=8383365; DOI=10.1016/0049-3848(93)90048-S;	RA Brothers A.B.; Clarke B.J.; Sheffield W.P.; Blaichman M.A.;
RT	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).	RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";	RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
RL	[2]	RL Thromb. Res. Suppl. 69:231-238(1993).	RL Thromb. Res. Suppl. 69:231-238(1993).
RN	RN [2]	RN [2]	RN [2]
RP	SEQUENCE FROM N.A.	RP REVISION TO 395.	RP REVISION TO 395.
RA	Hu Z., Garen A.; Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.	RC TISSUE=liver;	RC TISSUE=liver;
DR	EMBL; AF272774; AAC586862; -.	RA Ruiz S.R.; Blaichman M.A.; Clarke B.J.;	RA Ruiz S.R.; Blaichman M.A.; Clarke B.J.;
DR	HSSP; P08709; IKL1;	RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR	GO; GO:0005576; C:extracellular; IEA.	CC -I- FUNCTION: Initiates the extrinsic pathway of blood coagulation.	CC -I- FUNCTION: Initiates the extrinsic pathway of blood coagulation.
DR	GO; GO:0005509; F:calcium ion binding; IEA.	CC Serine protease that circulates in the blood in a zymogen form.	CC Serine protease that circulates in the blood in a zymogen form.
DR	GO; GO:0002833; F:peptidase activity; IEA.	CC Factor VII is converted to factor VIIa by Factor Xa, Factor Xla, Factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, Factor VIIa then converts Factor X to Factor Xa by limited proteolysis. Factor VIIa will also convert Factor IX to Factor IXa in the presence of tissue factor and calcium (By similarity).	CC Factor VII is converted to factor VIIa by Factor Xa, Factor Xla, Factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, Factor VIIa then converts Factor X to Factor Xa by limited proteolysis. Factor VIIa will also convert Factor IX to Factor IXa in the presence of tissue factor and calcium (By similarity).
DR	GO; GO:0004295; F:trypsin activity; IEA.	CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- Ile bond in Factor X to form Factor Xa.	CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- Ile bond in Factor X to form Factor Xa.
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	CC -I- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).	CC -I- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).
DR	InterPro; IPR00152; ASX-hydroxy_S.	CC -I- TISSUE SPECIFICITY: Plasma.	CC -I- TISSUE SPECIFICITY: Plasma.
DR	InterPro; IPR000742; EGF_2.	CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).	CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).
DR	InterPro; IPR001881; EGF_Ca.	CC -I- SIMILARITY: Belongs to the peptidase S1 family.	CC -I- SIMILARITY: Belongs to the peptidase S1 family.
DR	InterPro; IPR006209; EGF_Like.	CC -I- SIMILARITY: Contains 2 EGF-like domains.	CC -I- SIMILARITY: Contains 2 EGF-like domains.
DR	InterPro; IPR007110; Ig_Like.	CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla).	CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla).
DR	InterPro; IPR003597; Ig_c1.	CC	CC
DR	InterPro; IPR003006; Ig_KHC.	CC	CC
DR	InterPro; IPR001254; Peptidase_S1.	CC	CC
DR	InterPro; IPR009003; Pept_Ser_Cys.	CC	CC
DR	InterPro; IPR00294; Vitk_dep_GLA.	CC	CC
PFam	PF007654; C1-set; 2.	CC	CC
DR	PFam; PF00008; EGF_1.	CC	CC
DR	PFam; PF00594; Gla_1.	CC	CC
DR	PFam; PF00089; Trypsin_1.	CC	CC
SMART	SMART; S000179; BGP_Ca_1.	CC	CC
DR	SMART; S000069; GLA_1.	CC	CC
SMART	SMART; S0000407; IgC1_1.	CC	CC
DR	SMART; S000020; TRYPSIN_SPC_1.	CC	CC
DR	PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.	CC	CC
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.	CC	CC
DR	PROSITE; PS01186; EGF_2; 1.	CC	CC
DR	PROSITE; PS50026; EGF_3; 1.	CC	CC
DR	PROSITE; PS01187; EGF_CA_1.	CC	CC
DR	PROSITE; PS00011; GLA_1; 1.	CC	CC
DR	PROSITE; PS50035; Ig_LIKE_1.	CC	CC
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	CC	CC
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.	CC	CC
DR	PROSITE; PS00135; TRYPSIN_SER_1.	CC	CC
KW	EGF-like domain; Hydrolase; Protease; Serine protease.	CC	CC
SQ	SEQUENCE 679 AA; 75552 MW; 0B0023AA70A07A1 CRC64;	CC	CC

DR	InterPro; IPR006209; EGF-like.	Qy	1 ANAYFLXXLRPGSLXRCXXQCSPXXARXIFKDAKRTKLFWISY	5
DR	InterPro; IPR002383; GLA_blood.	Db	42 ANS-LIIEELMPGSLRECNNEQCSPEAREIFKSPERTKQFWIVY	85
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR001314; Peptidase_S1A.			
DR	InterPro; IPR009003; Pept_Ser_Cys.			
DR	InterPro; IPR000294; VitK_dep_GLA.			
DR	Pfam; PF00594; EGF; 2.			
DR	Pfam; PF00089; Trypsin; 1.			
DR	PRINTS; PR00722; CHMOTRYSIN.			
DR	PRINTS; PR00010; EGGBLOOD.			
DR	PRINTS; PR00001; GLABLOOD.			
DR	SMART; SMART_00179; EGF_CA; 1.			
DR	SMART; SMART_00069; GLA; 1.			
DR	SMART; SMART_00020; TRYSPC; 1.			
DR	PROSITE; PS00010; ASX HYDROXYL; 1.			
DR	PROSITE; PS00022; EGF_X; 1.			
DR	PROSITE; PS01186; EGF_2; FALSE_NEG.			
DR	PROSITE; PS00026; EGF_3; 1.			
DR	PROSITE; PS01187; EGF_CA; 1.			
DR	PROSITE; PS00011; GLA_-1; 1.			
DR	PROSITE; PS00998; GLA_2; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	Blood coagulation: Calcium-binding: EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation; Kappa chain repeat: Serine protease; Signal; Vitamin K; Zymogen.			
KW				
FT	SIGNAL 1 24			
FT	PROPEP 25 41			
FT	CHAIN 42 193			
FT	DOMAIN 194 446			
FT	DOMAIN 42 86			
FT	DOMAIN 87 123			
FT	DOMAIN 128 169			
FT	DOMAIN 194 446			
FT	SITE 193 194			
FT	ACT_SITE 234 234			
FT	ACT_SITE 283 283			
FT	ACT_SITE 385 385			
FT	BINDING 379 379			
FT	DISULFID 58 63			
FT	DISULFID 91 102			
FT	DISULFID 96 111			
FT	DISULFID 113 122			
FT	DISULFID 132 143			
FT	DISULFID 139 153			
FT	DISULFID 155 168			
FT	DISULFID 176 303			
FT	DISULFID 200 205			
FT	DISULFID 219 235			
FT	DISULFID 351 370			
FT	DISULFID 381 409			
FT	MOD_RES 47 47			
FT	MOD_RES 48 48			
FT	MOD_RES 55 55			
FT	MOD_RES 57 57			
FT	MOD_RES 60 60			
FT	MOD_RES 61 61			
FT	MOD_RES 66 66			
FT	MOD_RES 67 67			
FT	MOD_RES 70 70			
FT	MOD_RES 76 76			
FT	MOD_RES 104 104			
FT	CARBHYD 186 186			
FT	CARBHYD 244 244			
FT	CONFLICT 99 99		G -> V (in Ref. 2).	
SQ	SEQUENCE 446 AA; 50276 MW;		2512E44A5CBC96E CRC64;	
Query Match Score	58.5%		Length 446;	
Best Local Similarity	57.8%		Pred. No. 8.2e-12;	
Matches 26; Conservative 1; Mismatches 17; Indels 1; Gaps 1;				

DR	InterPro; IPR001314; Peptidase_S1A.
DR	InterPro; IPR009004; Pept_Ser_Cys.
DR	InterPro; IPR000294; VitK_dep_GLA.
DR	Pfam; PF00008; EGF; 2.
DR	Pfam; PF00094; Glu; 1.
DR	Pfan; PF00089; Trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPsin.
DR	PRINTS; PR00010; EGF_BLOOD.
DR	PRINTS; PR00001; GRABLOOD.
DR	SMART; SM00179; EGF_CA; 1.
DR	SMART; SM00069; GLP; 1.
DR	SMART; SM00020; TRYPSIN; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS00186; EGF_2; 2.
DR	PROSITE; PS00026; EGF_3; 1.
DR	PROSITE; PS01187; EGF_CA; 1.
DR	PROSITE; PS00011; GLA_1; 1.
DR	PROSITE; PS50998; GLA_2; 1.
DR	PROSITE; PS0040; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SSR; 1.
KW	Blood coagulation; Calcium-binding; Direct protein sequencing;
KW	EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase;
KW	Plasma; Repeat; Serine protease; Vitamin K; Zymogen.
PT	CHAIN 1 152 Factor VII light chain.
FT	CHAIN 1 407 Factor VII heavy chain.
FT	DOMAIN 1 45 Glu.
FT	DOMAIN 46 82 EGF-like 1, calcium-binding (Potential).
FT	DOMAIN 87 128 EGF-like 2.
FT	BINDING 338 338 Substrate (By similarity).
FT	DOMAIN 153 407 Serine protease.
FT	SITE 152 153 Cleavage by factor Xa, factor XIIa, factor IXa, or thrombin.
FT	ACT SITE 193 193 By similarity.
FT	ACT SITE 242 242 By similarity.
FT	ACT SITE 344 344 By similarity.
FT	BINDING 338 338 Substrate (By similarity).
FT	DISULFID 17 22 By similarity.
FT	DISULFID 50 61 By similarity.
FT	DISULFID 55 70 By similarity.
FT	DISULFID 72 81 By similarity.
FT	DISULFID 91 102 By similarity.
FT	DISULFID 98 112 By similarity.
FT	DISULFID 114 127 By similarity.
FT	DISULFID 135 262 By similarity.
FT	DISULFID 159 164 By similarity.
FT	DISULFID 178 194 By similarity.
FT	DISULFID 310 329 By similarity.
FT	DISULFID 340 368 By similarity.
FT	MOD_RES 6 6 -carboxyglutamate.
FT	DISULFID 7 7 4-carboxyglutamate.
FT	MOD_RES 14 14 4-carboxyglutamate.
FT	MOD_RES 16 16 4-carboxyglutamate.
FT	DISULFID 19 19 4-carboxyglutamate.
FT	MOD_RES 20 20 4-carboxyglutamate.
FT	MOD_RES 25 25 4-carboxyglutamate.
FT	MOD_RES 26 26 4-carboxyglutamate.
FT	MOD_RES 29 29 4-carboxyglutamate.
FT	MOD_RES 35 35 4-carboxyglutamate.
FT	CARBOHYD 52 52 O-linked (Glc . . .).
FT	CARBOHYD 145 145 N-linked (GlcNAc . . .).
FT	CARBOHYD 203 203 N-linked (GlcNAc . . .).
SQ	SEQUENCE 407 AA; 44431 MW; 703E1F506367F10 CRC4;
Query Match	56.8%; Score 113; DB 1; Length 407;
Best Local Similarity	51.2%; Pred. No. 3.1e-11;
Matches 21;	Conservative 5; Mismatches 15; Indels 0; Gaps 0;
Qy	5 FLXXLRPGSLIURXCKXQCSFXKXARXIFKDAKRTKLFWIY 45
Db	4 FLEELBLPGSLERECREELCSSEEAEIFPRNEERTQFWVSY 44
RESULT 7	
PRC_PIG	STANDARD;
ID	PRTC_PIG
AC	O9GLB2;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)

RESULT 6	
QBOTHC9	PRELIMINARY;
ID	OBJHC9
AC	Q8THC9;
DT	01-OCT-2002 (TRIMBLrel. 22, Created)
DT	01-OCT-2002 (TRIMBLrel. 22, Last sequence update)
DT	05-JUL-2004 (TRIMBLrel. 27, Last annotation update)
DE	Coagulation factor VIII.
GN	Name=F7;
OS	Brachydanio rerio (Zebrafish) (<i>Danio rerio</i>).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TAXID	NCBI_TAXID=7955;
RN	[1]
RP	SEQUENCE FROM N_A.
RA	Hanumantahal R., Day K., Jagadeeshwar P.;
RT	"Comprehensive analysis of blood coagulation pathways in Teleostei:
RT	Evolution of coagulation factor genes and identification of zebrafish
RL	Factor VIII.";
RT	Blood Cells Mol. Dis. 0:0-0(2002).
CC	- - SIMILARITY: Belongs to peptidase family S1.
CC	- - SIMILARITY: Contains 1 EGF-like domain.
DR	EMBL; AF515269; AAN71000.1; -.
DR	EMBL; AF515269; AAN71000.1; -.
DR	HSSP; P00744; 1CPH.
DR	ZFIN; ZDB-GENE-021206-10; f7i.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005509; F:calcium ion binding; IBA.
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0008233; F:peptidase activity; IEA.
DR	GO; GO:0004295; F:peptidase activity; IEA.
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR	InterPro; IPR00742; EGF_2.
DR	DR InterPro; IPR006209; EGF-like.
DR	DR InterPro; IPR00383; GLA_blood.
DR	DR InterPro; IPR00210; IEGF.
DR	DR InterPro; IPR004254; Peptidase_S1.
DR	DR InterPro; IPR00314; Peptidase_SIA.
DR	DR InterPro; IPR009003; Pept_Ser_Cys.
DR	DR InterPro; IPR00294; VitK_dep_GLA.
Pfam	Pfam; PF00098; BCF; 1.
Pfam	Pfam; PF00594; GLA; 1.
DR	DR PROSITE; PS00002; TRYSPN; 1.
DR	DR PROSITE; PS00089; TRYSPN; 1.
DR	DR PRINTS; PR00722; CHYNOTRYPSIN.
DR	DR PRINTS; PR00001; GLABLOOD.
DR	DR SMART; SM00181; EGF; 2.
DR	DR SMART; SM00069; GLA; 1.
DR	DR SMART; SM00020; TRYSPN; 1.
DR	DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	DR PROSITE; PS00026; EGF_2; 2.
DR	DR PROSITE; PS00026; EGF_3; 1.
DR	DR PROSITE; PS00011; CLA_1; 1.
DR	DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR	DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW	EGF-like domain; Hydrolase; Protease; Serine protease.
SQ	SEQUENCE 443 AA; 48823 MW; 2D254718LE94FF4 CR64;
Query Match	54.8%; Score 109; DB 2; Length 443;
Best Local Similarity	44.4%; Pred. No. 1.8e-10;
Matches 20;	Conservative 8; Mismatches 17; Indels 0; Gaps 0;
Qy	1 ANAYFLXXLRPGSLIURXCKXQCSFXKXARXIFKDAKRTKLFWIY 45
Db	38 ANSGFLEMKAQNLERBCVEETCDYEAREVFFDDDTKQFNLSY 82

25-OCT-2004 (Rel. 45, Last annotation update)
 Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).

DE PROSITE; PS01186; EGF_2; 2.
 DE PROSITE; PS50026; EGF_CN; 1.
 DE PROSITE; PS01187; EGF_CN; 1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS50098; GLA_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SSR; 1.
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine protease; Signal; Vitamin K.
 FT SIGNAL_1 18
 FT PROPP_1 18
 FT CHAIN_1 18
 FT CHAIN_42 196
 FT PEPTIDE_1 199
 FT SITE_213 213
 FT DOMAIN_42 87
 FT DOMAIN_96 131
 FT DOMAIN_135 175
 FT DOMAIN_214 459
 FT MOD_RES_47 47
 FT MOD_RES_48 48
 FT MOD_RES_55 55
 FT MOD_RES_57 57
 FT MOD_RES_60 60
 FT MOD_RES_61 61
 FT MOD_RES_66 66
 FT MOD_RES_67 67
 FT MOD_RES_70 70
 FT MOD_RES_112 112
 FT ACT_SITE_255 255
 FT ACT_SITE_301 301
 FT ACT_SITE_400 400
 FT DISUFID_58 63
 FT DISUFID_91 110
 FT DISUFID_100 105
 FT DISUFID_104 119
 FT DISUFID_121 130
 FT DISUFID_139 150
 FT DISUFID_146 159
 FT DISUFID_161 174
 FT DISUFID_182 221
 FT DISUFID_240 256
 FT DISUFID_371 385
 FT CARBOHYD_396 424
 FT CARBOHYD_138 138
 FT CARBOHYD_292 292
 FT CARBOHYD_353 353
 SQ SEQUENCE_459 AA; MW; 6541AAC14CC16D09 CRC64;

Query Match 52.0%; Score 103.5; DB 1; Length 459;
 Best Local Similarity 48.9%; Pred. No. 1..7e-09;
 Matches 22; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

CC SEQUENCE FROM N.A.
 CC TISSUE=Liver;
 CC MEDLINE=2121490; PubMed=11229814;
 RA Grimm D.R.; Colter M.B.; Braunschweig M.; Alexander L.J.; Neame P.J.; Kim H.K.W.;
 RA "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains";
 RT Cell. Mol. Life Sci. 58:148-159 (2001).
 CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIa in the presence of calcium ions and phospholipids.
 CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIa.
 CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetrapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
 CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
 CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GlA domain. This GlA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AP91307; AA28280.1; -.
 DR MEROPS; S01_21.8; -.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006509; EGF_Like.
 DR InterPro; IPR002388; GLA_Blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR009003; Pept_Ser_Cys.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000294; VitK_dep_Gla.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; Gla_1.
 DR Pfam; PF0000; Trypsin; 1.
 DR PRINTS; PRO00001; GLABLOOD.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; TRYSPC_1.
 DR PROSITE; PS00010; ASX_HYDROXYL_1.
 DR PROSITE; PS00022; EGF_1; 1.

RESULT 8
 PRTC_MOUSE STANDARD; PRT; 460 AA.
 ID PRTC_MOUSE_ID P33587; O35498; Q99BC6;
 AC 01-FEB-1994 (Rel. 28, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Vitamin K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).

GN Name=Proc;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=BALB/C; TISSUE=Liver;
 RC MEDLINE=02316897; PubMed=1618739;
 RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
 RT "Isolation and characterization of a mouse protein C cDNA.";
 RL J. Biochem. 111:491-495(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ;
 RX MEDLINE=98152576; PubMed=9493582;
 RA Jalbert L.R., Rosen B.D., Lissens A., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Nucleotide structure and characterization of the murine gene encoding
 anticoagulant protein C.";
 RL Thromb. Haemost. 79:310-316(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Korf I.;
 RT "Completed sequence of UC72A01.";
 RL Submitted (Nov-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=02388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schaefer C.F., Bhat N.K.,
 RA Shemer C.M., Shuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Wagner L., Shenmen C.M.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udin T.B., Toshiyuki S., Carminci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulilal S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S.A.M., Worley K.C., Hale S., Garcia R.A.,
 RA Villalon D.K., Muny D.M., Soderren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Heiton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Smilus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marrs M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 274-433 FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=14318474; PubMed=8043441;
 RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihon Y.;
 RT "A comparative study of partial primary structures of the catalytic
 region of mammalian protein C.";
 RT Br. J. Haematol. 86:590-600(1994).
 CC -I- FUNCTION: Protein C is a vitamin K-dependent serine protease that
 CC regulates blood coagulation by inactivating factors Va and VIIa
 CC in the presence of Calcium ions and phospholipids.
 CC -I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -I- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
 CC into a light chain and a heavy chain held together by a disulfide
 CC bond. The enzyme is then activated by thrombin, which cleaves a
 CC tetrapeptide from the amino end of the heavy chain; this
 CC reaction, which occurs at the surface of endothelial cells, is
 CC strongly promoted by thrombomodulin.
 CC -I- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.

CC -I- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GlA domain. This GlA-independent binding
 CC site is necessary for the recognition of the thrombin-
 CC thrombomodulin complex.
 CC -I- SIMILARITY: Belongs to the peptidase S1 family.
 CC -I- SIMILARITY: Contains 2 EGF-like domains.
 CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.ebi-sib.ch/announce/>
 CC or send an email to licenses@ebi-sib.ch.)
 CC DR EMBL: D10445; BRA01235; 1;
 CC DR EMBL: AF034569; AAC33795; 1;
 CC DR EMBL: AF318182; AAK07918; 1;
 CC DR EMBL: BC013896; AAH13896; 1;
 CC DR EMBL: D43755; BRA007812; 1;
 CC DR PIR: JX0210; JX0210;
 CC DR HSSP: P04070; IAUT;
 CC DR MEROPS: S01; 218; 1;
 CC DR MGB: MGJ:97771; PROC;
 CC DR InterPro: IPR00152; ASX hydroxyl_S;
 CC DR InterPro: IPR000742; EGF_2;
 CC DR InterPro: IPR001881; EGF_2a;
 CC DR InterPro: IPR000209; EGF like;
 CC DR InterPro: IPR002383; GLA_blood;
 CC DR InterPro: IPR000303; Pept_Ser_Cys;
 CC DR InterPro: IPR001254; Peptidase_S1;
 CC DR InterPro: IPR000314; Peptidase_S1A;
 CC DR InterPro: IPR000394; VitK_dep_Gla;
 CC DR Pfam: PF00068; EGF_2;
 CC DR Pfam: PF00594; GLA_1;
 CC DR PRINTS: PR00722; CHYNOTRYPSIN;
 CC DR PRINTS: PR00001; GLABLOOD;
 CC DR SMART: SM00069; GLA_1;
 CC DR SMART: SM00020; Tryp_SPC_1;
 CC DR PROSITE: PS00010; ASX_HYDROXYL_1;
 CC DR PROSITE: PS00022; EGF_1; 1;
 CC DR PROSITE: PS01186; EGF_2; 2;
 CC DR PROSITE: PS00026; EGF_3; 1;
 CC DR PROSITE: PS01187; EGF_CA_1;
 CC DR PROSITE: PS00011; GLA_1; 1;
 CC DR PROSITE: PS05098; GLA_2; 1;
 CC DR PROSITE: PS00240; TRYPsin_DOM; 1;
 CC DR PROSITE: PS00134; TRYPsin_HIS; 1;
 CC DR PROSITE: PS00135; TRYSIN_SER; 1;
 KW Blood coagulation; Calcium-binding; EGF-like domain;
 KW Gamma-carboxyglutamic acid; Glycoprotein; Hydrolase; Hydroxylation;
 KW Repeat; Serine Protease; Signal; Vitamin K;
 FT SIGNAL 1 33 By similarity.
 FT PROPEP 34 41 By similarity.
 FT CHAIN 42 460 Vitamin K-dependent protein C.
 FT CHAIN 42 196 Vitamin K-dependent protein C light chain
 FT CHAIN 199 460 Vitamin K-dependent protein C heavy chain
 FT PEPTIDE 199 212 Activation Peptide (By similarity).
 FT SITE 212 213 Cleavage (by thrombin) (By similarity).
 FT DOMAIN 42 87 GlA.
 FT DOMAIN 96 131 EGF-like 1.
 FT DOMAIN 135 175 EGF-like 2.
 FT DOMAIN 213 460 Serine protease.
 FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
 FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
 FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
 CC 57 57 4-carboxyglutamate (By similarity).

RL Biochem. J. 351:557-565 (2000).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- PTM: Glu residues are produced after subsequent posttranslational
 CC modifications of glutamate by a vitamin K-dependent gamma-
 CC carboxylase (By similarity).
 CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; BC225098; AAH25098.1; -.
 DR EMBL; AF20205; AAC44244.1; -.
 DR HSSP; P0740; 1CFH.
 DR MGD; MG11929596; Frrg2.
 DR GO:0005515; F-protein binding; IPI.
 DR InterPro; IPR002385; GLA_blood.
 DR InterPro; IPR000294; VitK_dep,GLA.
 DR Pfam; PF00594; Gla_1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA_1.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS50598; GLA_2; 1.
 KW Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.
 FT SIGNAL 1 20 Potential.
 FT PROPEP 21 51 By similarity.
 FT CHAIN 52 198 Transmembrane gamma-carboxyglutamic acid
 protein 2.
 FT DOMAIN 52 111 Extracellular (Potential).
 FT TRANSMEM 112 134 Potential.
 FT DOMAIN 135 198 Cytoplasmic (Potential).
 FT DOMAIN 52 97 Gla.
 SQ SEQUENCE 198 AA; 22369 MW; 1C6482C8445450FC CRC64;
 Query Match 48.2%; Score 96; DB 1; Length 198;
 Best Local Similarity 44.4%; Pred. No. 1.6e-08;
 Matches 20; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 ANAYFLXXLRPGSLRXCXQXXPSXKFDAXRTKLFWTSY 45
 Db 52 ANHWDLLELTPGNLRECLERCWSWEAREYFEDNTLIERFWTSY 96

RESULT 11
 TMG2 HUMAN STANDARD; PRT; 202 AA.
 ID TMG2_HUMAN STANDARD; PRT; 202 AA.
 AC 014659; Q6D1H4; PRELIMINARY;
 DT 28-FEB-2003 (Rel. 41, Created) PRT; 216 AA.
 DT 28-FEB-2003 (Rel. 41, Last sequence update) Q6D1H4
 DT 05-JUL-2004 (Rel. 44, Last annotation update) AC
 DE Transmembrane Gamma-carboxyglutamic acid protein 2 precursor (proline-rich Gla protein 2) (Proline-rich gamma-carboxyglutamic acid protein 2).
 DE Name=PRGP2; Synonyms=PRGP2, TMG2;
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] Q6D1H4
 RP SEQUENCE FROM N.A.
 RX MEDLINE=040347; PubMed=9256434; DOI=10.1073/pnas.94.17.9058;
 RA Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
 RT "Primary structure and tissue distribution of two novel proline-rich
 gamma-carboxyglutamic acid proteins."
 RT Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062 (1997).
 CC -1- SUBUNIT: Binds NEDD4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: Highly expressed in the thyroid.
 CC -1- PTM: Glu residues are produced after subsequent posttranslational
 CC modifications of glutamate by a vitamin K-dependent gamma-
 CC carboxylase.
 CC -1- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
 CC domain.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AF009243; AAB67071.1; -.
 DR HSSP; P00740; 1CFH.
 DR Gene; HGNC:9470; PRRG2.
 DR MIM; 604429; -.
 DR GO:0005587; C:integral to plasma membrane; TAS.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR11047; Quin_acic_DH_like.
 DR InterPro; IPR00094; VitK_dep,GLA.
 DR Pfam; PF00594; Gla_1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA_1.
 DR PROSITE; PS50998; GLA_2; 1.
 DR PROSITE; PS55099; Gamma-carboxyglutamic acid; Signal; Transmembrane; Vitamin K.
 DR SIGNAL 1 23 Potential.
 FT PROPEP 24 49
 FT CHAIN 50 202 Transmembrane gamma-carboxyglutamic acid protein 2.
 FT DOMAIN 50 109 Extracellular (Potential).
 FT TRANSMEM 110 132 Potential.
 FT DOMAIN 133 202 Cytoplasmic (Potential).
 FT DOMAIN 50 96 Gla.
 FT DOMAIN 161 173 Poly-Pro.
 FT DOMAIN 191 194 Poly-Pro.
 SQ SEQUENCE 202 AA; 22393 MW; BC79400C98492060 CRC64;
 Query Match 48.2%; Score 96; DB 1; Length 202;
 Best Local Similarity 44.4%; Pred. No. 1.6e-08;
 Matches 6; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 ANAYFLXXLRPGSLRXCXQXXPSXKFDAXRTKLFWTSY 45
 Db 50 ANHWDLLELTPGNLRECLERCWSWEAREYFEDNTLIERFWTSY 94

RESULT 12
 Q6D1H4
 ID Q6D1H4; PRELIMINARY;
 AC Q6D1H4; PRT; 216 AA.
 DT 25-OCT-2004 (TRIMBLrel. 28, Created)
 DT 25-OCT-2004 (TRIMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRIMBLrel. 28, Last annotation update)
 DE Prgr4_prov protein.
 DE Name=prg4_prov;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=3364;
 RN [1] Q6D1H4
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubhaar R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmee C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B.R., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.S., McIwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.P., Wahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grindwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailius D.E., Schnarch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	DR	InterPro; IPR006210; IEGF.
[2]	SEQUENCE FROM N.A.	DR	InterPro; IPR001254; Peptidase_S1.
RC	TISSUE=Embryo;	DR	InterPro; IPR01314; Peptidase_S1A.
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	DR	InterPro; IPR009003; Pept_Ser_Cys.
RL	EMBL; BC075566; AAH55566_1;	DR	InterPro; IPR000294; VitK_dep_GLA.
DR	GO: GO:0005576; C: extracellular; IBA.	PFam;	PF00008;
DR	GO: GO:005509; F: calcium ion binding; IEA.	PFam;	PF00594;
InterPro	IPIR002383; GLA_blood.	DR	Pfam; PF00089;
DR	IPR000294; VitK_dep_GLA.	DR	Pfam; PF00089;
PFam	PF00594; GLa; 1.	DR	PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS	PR00089; Trypsin; 1.	DR	PRINTS; PR00722; CHYMOTRYPSIN.
RN	RP000181; EGF; 2.	DR	PRINTS; PR000181; GLABLOOD.
RC	SMART; SM00089; GLA; 1.	DR	SMART; SM00089; GLA; 1.
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	DR	SMART; SM00030; TRYSP_SPC; 1.
RA	EMBL; BC075566; AAH55566_1;	DR	PROSITE; PS000022; EGF; 1;
DR	GO: GO:0005576; C: extracellular; IBA.	DR	PROSITE; PS01186; EGF; 2.
DR	GO: GO:005509; F: calcium ion binding; IEA.	DR	PROSITE; PS50026; EGF; 3.
DR	InterPro; IPIR002383; GLA_blood.	DR	PROSITE; PS50011; GLA; 1; 1.
DR	IPR000294; VitK_dep_GLA.	DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PFam; PF00594; GLa; 1.	DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
PRINTS	PR00001; GLABLOOD.	KW	EGL-like domain; Hydrolase; Protease; Serine protease.
DR	PROSITE; PS00011; GLA; 1.	SEQUENCE	442 AA; 48/87 MW; 810A561A127P0CF7 CRC64;
SQ	SEQUENCE FROM N.A.	SO	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;	Query Match	47.2%; Score 94; DB 2; Length 442;
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	Best Local Similarity	37.8%; Pred. No. 8.2e-08;
RL	EMBL; BC075566; AAH55566_1;	Matches	11; Mismatches 17; Indels 0; Gaps 0;
DR	GO: GO:0005576; C: extracellular; IBA.	DR	GO: GO:0005576; C: extracellular; IBA.
DR	GO: GO:005509; F: calcium ion binding; IEA.	DR	GO: GO:005509; F: calcium ion binding; IEA.
DR	InterPro; IPIR002383; GLA_blood.	DR	InterPro; IPIR002383; GLA_blood.
DR	IPR000294; VitK_dep_GLA.	DR	IPR000294; VitK_dep_GLA.
PFam	PF00594; GLa; 1.	DR	PFam; PF00089;
PRINTS	PR00001; GLABLOOD.	DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PROSITE; PS00011; GLA; 1.	DR	PROSITE; PS50026; EGF; 3.
DR	PROSITE; PS00011; GLA; 1.	DR	PROSITE; PS50011; GLA; 1.
DR	PROSITE; PS00011; GLA; 1.	DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
SQ	SEQUENCE 216 AA; 23721 MW; 790D18DDA229087A CRC64;	DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
RESULT 14	RESULT 14	DR	PROSITE; PS00011; GLA; 1.
Query Match	47.7%; Score 95; DB 2; Length 216;	DR	PROSITE; PS00011; GLA; 1.
Best Local Similarity	36.4%; Pred. No. 2.6e-08;	DR	PROSITE; PS00011; GLA; 1.
Matches	20; Conservative 8; Mismatches 17; Indels 10; Gaps 1;	DR	PROSITE; PS00011; GLA; 1.
DR	GO: GO:0005576; C: extracellular; IBA.	DR	PROSITE; PS00011; GLA; 1.
DR	GO: GO:005509; F: calcium ion binding; IEA.	DR	PROSITE; PS00011; GLA; 1.
DR	InterPro; IPIR002383; GLA_blood.	DR	PROSITE; PS00011; GLA; 1.
DR	IPR000294; VitK_dep_GLA.	DR	PROSITE; PS00011; GLA; 1.
PFam	PF00594; GLa; 1.	DR	PROSITE; PS00011; GLA; 1.
PRINTS	PR00001; GLABLOOD.	DR	PROSITE; PS00011; GLA; 1.
DR	PROSITE; PS00011; GLA; 1.	DR	PROSITE; PS00011; GLA; 1.
SQ	SEQUENCE 216 AA; 23721 MW; 790D18DDA229087A CRC64;	DR	PROSITE; PS00011; GLA; 1.
RESULT 15	RESULT 15	DR	PROSITE; PS00011; GLA; 1.
Q800X1	Q800X1 PRELIMINARY; PRT; 442 AA.	DR	PROSITE; PS00011; GLA; 1.
ID	Q800X1 ID Q800X7 PRELIMINARY; PRT; 425 AA.	DR	PROSITE; PS00011; GLA; 1.
AC	Q800X1 AC Q800X7 PRELIMINARY; PRT; 442 AA.	DR	PROSITE; PS00011; GLA; 1.
DT	01-JUN-2003 (TREMBREL. 24, Created)	DR	PROSITE; PS00011; GLA; 1.
DT	01-JUN-2003 (TREMBREL. 24, Last sequence update)	DR	PROSITE; PS00011; GLA; 1.
DT	01-MAR-2004 (TREMBREL. 26, Last annotation update)	DR	PROSITE; PS00011; GLA; 1.
DR	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
NCBI_TaxID	3103; HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
OC	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RA	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
DR	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
OC	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RA	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
DR	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
OC	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RA	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
DR	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P00709; 1_KLJ.	DR	PROSITE; PS00011; GLA; 1.
RN	SEQUENCE FROM N.A.	DR	PROSITE; PS00011; GLA; 1.
RP	Davidson C.J., Hirai R.P., Lal K., Snell P., Elgar G., Tuddenham E.G.D., McEvay J.H., Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS00011; GLA; 1.
RA	Coagulation factor VIII (EC 3.4.21.21)	DR	PROSITE; PS00011; GLA; 1.
DR	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).	DR	PROSITE; PS00011; GLA; 1.
DB	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Osteichthyes; Acanthopterygii; Percomorpha; Tetraodontiformes; Osteichthyes; Tetraodontidae; Takifugu.	DR	PROSITE; PS00011; GLA; 1.
CC	- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
CC	-- SIMILARITY: Belongs to peptidase family S1.	DR	PROSITE; PS00011; GLA; 1.
DR	EMBL; AF065274; AAC033369.1; -.	DR	PROSITE; PS00011; GLA; 1.
DR	HSSP; P		

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR PFam; PF00594; Gla; 1.
PFam; PF00089; Trypsin; 1.
DR PRINTS; PRO0022; CHYMOTRYPSIN.
DR PRINTS; PRO0010; EGF_BLOOD.
DR PRINTS; PRO0001; GLABLOOD.
DR SMART; SMART001; EGF; 2.
SMART; SMART0069; GLA; 1.
DR SMART; SMART0020; TRYSP_SPC; 1.
DR PROSITE; PS00110; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS00187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGFR-like domain; Hydrolase; Protease; Serine protease;
SEQUENCE 425 AA; 47626 MW; 36A69BF0DBC6DAC CRC64;
SQ

Query Match 47.0%; Score 93.5%; DB 2; Length 425;
Best Local Similarity 44.4%; Pred. No. 9.4e-08;
Matches 20; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRCKXQCSFXKAXTFLKFLWISY 45
Db 41 ANSFP-EEIKLGPPLERECIEKCSFEAREI YRDDERTKEFWHY 84

RESULT 15

FA7_RAT	FA7_RAT	STANDARD;	PRT;	446 AA.
AC Q8K3U6;				
DT 05-JUL-2004 (Rel. 44, Created)				
DT 05-JUL-2004 (Rel. 44, Last sequence update)				
DT 25-OCT-2004 (Rel. 45, Last annotation update)				
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).				
GN Rattus norvegicus (Rat).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.				
RN [1]				
RC SEQUENCE FROM N.A.				
RA Murphy K.; Ramaker M.;				
RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII."				
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.				
CC -I- FUNCTION: Initiates the extrinsic pathway of blood coagulation.				
CC -I- Serine protease that circulates in the blood in a zymogen form.				
CC Factor VII is converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor Xa by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium (By similarity).				
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg- -Ile bond in factor X to form factor Xa.				
CC -I- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by a disulfide bond (By similarity).				
CC -I- TISSUE SPECIFICITY: Plasma.				
CC -I- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By similarity).				
CC -I- SIMILARITY: Belongs to the peptidase S1 family.				
CC -I- SIMILARITY: Contains 2 EGF-like domains.				
CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla).				
CC -I- This SWISS-PROT entry is copyrighted. It is produced through collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -				
DR EMBL; AF532184; AAC95967.1; -.				
DR HSPP; P08709; 1KLJ.				
DR DR InterPro; IPR002086; Aldehyde_dehydr.				
DR DR InterPro; IPR001052; Asx_hydroxyl_S.				
DR DR InterPro; IPR001042; EGF_-2.				
DR DR InterPro; IPR001181; EGF_Ca.				
DR DR InterPro; IPR001138; EGF_II.				
DR DR InterPro; IPR006209; EGF_-like.				
DR DR InterPro; IPR002383; GLA_blood.				
DR DR InterPro; IPR001234; Peptidase_S1.				
DR DR InterPro; IPR001314; Peptidase_SIA.				
DR DR InterPro; IPR009003; Pept_Ser_Cys.				
DR DR InterPro; IPR000294; VitK_dep_GLIA.				
DR Pram; PF000594; EGF; 2.				
DR Pram; PF000594; Trypsin; 1.				
DR PRNTS; PR00722; CHYMOTRYPSIN.				
DR PRNTS; PR00110; EGF_BLOOD.				
DR PRNTS; PR00001; GLABL0OD.				
DR SMART; SM00179; EGF_CA; 1.				
DR SMART; SM00069; GLA; 1.				
DR SMART; SM00020; TRYSP_SPC; 1.				
DR PROSITE; PS00010; ASX_HYDROXYL; 1.				
DR PROSITE; PS00022; EGF_1; 1.				
DR PROSITE; PS00186; EGF_2; FALSE_NEG.				
DR PROSITE; PS00026; EGF_3; 1.				
DR PROSITE; PS00187; EGF_CA; 1.				
DR PROSITE; PS00098; GLA_1; 1.				
DR PROSITE; PS50240; TRYPSIN_DOM; 1.				
DR PROSITE; PS00134; TRYPSIN_HIS; 1.				
DR PROSITE; PS00135; TRYPSIN_SER; 1.				
KW Blood coagulation; Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Hydroxylase; Hydrolase; Vitamin K; Zymogen.				
KW Plasma; Repeat; Serine protease; Signal; Vitamin K; Zymogen.				
KW SIGNAL; 1				
FT PROTEP 24				
FT PROTEP 25				
FT CHAIN 41				
FT CHAIN 42				
FT CHAIN 194				
FT DOMAIN 446				
FT DOMAIN 42				
FT DOMAIN 87				
FT DOMAIN 128				
FT DOMAIN 194				
FT SITE 193				
FT ACT_SITE 234				
FT ACT_SITE 234				
FT ACT_SITE 283				
FT ACT_SITE 385				
FT BINDING 385				
FT DISULFID 379				
FT DISULFID 579				
FT DISULFID 63				
FT DISULFID 91				
FT DISULFID 102				
FT DISULFID 96				
FT DISULFID 111				
FT DISULFID 113				
FT DISULFID 122				
FT DISULFID 132				
FT DISULFID 139				
FT DISULFID 155				
FT DISULFID 168				
FT DISULFID 176				
FT DISULFID 200				
FT DISULFID 205				
FT DISULFID 219				
FT DISULFID 235				
FT DISULFID 351				
FT DISULFID 370				
FT MOD_RES 409				
FT MOD_RES 381				
FT MOD_RES 447				
FT MOD_RES 48				
FT MOD_RES 55				
FT MOD_RES 57				
FT MOD_RES 60				

```

PT      MOD_RES    61      61      4-carboxyglutamate (By similarity).
PT      MOD_RES    66      66      4-carboxyglutamate (By similarity).
PT      MOD_RES    67      67      4-carboxyglutamate (By similarity).
PT      MOD_RES    70      70      4-carboxyglutamate (By similarity).
PT      MOD_RES    76      76      4-carboxyglutamate (By similarity).
PT      MOD_RES   104     104     3-hydroxyaspartate (By similarity).
PT      CARBOHYD  186     186     N-linked (GlcNAc. . .) (Potential).
PT      CARBOHYD  244     244     N-linked (GlcNAc. . .) (Potential).
SQ      SEQUENCE  446 AA;  50399 MW;  292985EBF119COA CRC64;

Query Match Score 93.5; DB 1; Length 446;
Best Local Similarity 47.0%; Pred. No. 1e-07;
Matches 22; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

Qy      1 ANAYFLXXLRRPGSLXRXCKXXQCSEXXARKIFKDAXRTKLFWISY 45
Db      42 ANS-LLEELNSSLBRECNEBCSFBEARBTFKSPERTKQFWTLY 85

```

Search completed: August 22, 2005, 18:42:25
 Job time : 85 SECs

This Page Blank (uspto)

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 09:42:23 ; Search time 30 Seconds

(without alignments)
 111.974 Million cell updates/sec

Title: US10031005-3Y4

Perfect score: 199

Sequence: 1 ANAYFLXXLRPGLSLXRXCKX.....XXARXIFKDAXRTKLFWISY 45

Scoring table: BLOSUM62

Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
 1: /cgns_6/_ptodata/1/iaa/5A COMB.pep *
 2: /cgns_6/_ptodata/1/iaa/5B COMB.pep *
 3: /cgns_6/_ptodata/1/iaa/6A COMB.pep *
 4: /cgns_6/_ptodata/1/iaa/6B COMB.pep *
 5: /cgns_6/_ptodata/1/iaa/PEUTUS COMB.pep *
 6: /cgns_6/_ptodata/1/iaa/backfile1.pep :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	44	3 US-08-955-636-3	Sequence 3, Appli
2	161.5	81.2	44	4 US-09-302-239-3	Sequence 3, Appli
3	161.5	81.2	44	4 US-09-197-591-3	Sequence 3, Appli
4	161.5	81.2	44	4 US-09-190-803-1	Sequence 3, Appli
5	161.5	81.2	406	1 US-08-293-778-24	Sequence 24, Appli
6	161.5	81.2	406	1 US-08-195-111-5	Sequence 5, Appli
7	161.5	81.2	406	2 US-08-955-711-5	Sequence 5, Appli
8	161.5	81.2	406	4 US-09-782-587B-1	Sequence 1, Appli
9	161.5	81.2	406	4 PCT-US92-10242-5	Sequence 5, Appli
10	161.5	81.2	406	5 PCT-US92-10242-5	Sequence 5, Appli
11	161.5	81.2	444	1 US-08-475-845-2	Sequence 2, Appli
12	161.5	81.2	444	2 US-08-527-630-2	Sequence 2, Appli
13	161.5	81.2	444	2 US-08-660-889-2	Sequence 2, Appli
14	161.5	81.2	444	2 US-08-537-807-2	Sequence 2, Appli
15	161.5	81.2	444	2 US-08-871-003-2	Sequence 2, Appli
16	161.5	81.2	444	3 US-08-464-333-2	Sequence 2, Appli
17	161.5	81.2	444	3 US-09-189-607-2	Sequence 2, Appli
18	161.5	81.2	444	3 US-09-178-307-2	Sequence 2, Appli
19	161.5	81.2	444	5 PCT-US94-05779-2	Sequence 2, Appli
20	161.5	81.2	461	4 US-09-949-016-8839	Sequence 8839, Ap
21	161.5	81.2	466	1 US-07-882-002A-4	Sequence 4, Appli
22	161.5	81.2	466	1 US-08-021-615A-4	Sequence 4, Appli
23	161.5	81.2	466	1 US-08-321-277-4	Sequence 4, Appli
24	161.5	81.2	466	3 US-09-009-177-14	Sequence 14, Appli
25	161.5	81.2	466	3 US-09-009-656-14	Sequence 14, Appli
26	161.5	81.2	466	5 PCT-US93-0493-4	Sequence 4, Appli
27	161.5	81.2	483	4 US-09-949-016-9523	Sequence 9523, Ap

ALIGNMENTS

RESULT 1 US-08-955-636-3	Sequence 3, Application US/08955636A ; Patent No. 6017982 ; GENERAL INFORMATION: ; APPLICANT: Nelsetuen, Gary L. ; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT ; POLYPEPTIDES ; FILE REFERENCE: 09531/002001 ; CURRENT APPLICATION NUMBER: US/08/955, 636A ; CURRENT FILING DATE: 1999-10-23 ; NUMBER OF SEQ ID NOS: 35 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 3 ; LENGTH: 44 ; TYPE: PRT ; ORGANISM: Homo sapiens ; NAME/KEY: MOD_RES ; LOCATION: (0) .. (0) ; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-3
Query Match	81.2%; Score 161.5; Best Local Similarity 97.8%; Pred. No. 1.e-19; Mismatches 44; Conservative Matches 44; Indels 0; Gaps 1;
Qy	1 ANAYFLXXLRPGLSLXRXCXQCSFXARXIFKDXRTKLFWISY 45
Db	1 ANA-FLXXLRPGLSLXRXCXQCSFXARXIFKDXRTKLFWISY 44
RESULT 2 US-09-302-239-3	Sequence 3, Application US/09302239 ; Patent No. 6693075 ; GENERAL INFORMATION: ; APPLICANT: Nelsetuen, Gary L. ; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT ; POLYPEPTIDES ; FILE REFERENCE: 09531/002001 ; CURRENT APPLICATION NUMBER: US/09/302, 239 ; CURRENT FILING DATE: 1999-04-29 ; NUMBER OF SEQ ID NOS: 18 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 3 ; LENGTH: 44 ; TYPE: PRT ; ORGANISM: Homo sapiens ; FEATURE:

NAME/KEY: MOD_RES
 LOCATION: (0) ..(0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-302-239-3

Query Match Score 161.5; DB 4; Length 44;
 Best Local Similarity 97.8%; Pred. No. 1..le-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAVFLXXLRPGSLRXCXXQCSFXXXARXIFKDAVRTLFWI SY 45
 Db 1 ANA-FLXXLRPGSLRXCXXQCSFXXXARXIFKDAVRTLFWI SY 44

RESULT 3

US-09-497-591-3

Sequence 3, Application US/09497591
 Patent No. 6747003
 GENERAL INFORMATION:
 APPLICANT: Nelestuen, Gary L.
 TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
 TITLE OF INVENTION: POLYPEPTIDES
 FILE REFERENCE: 9531-016001
 CURRENT APPLICATION NUMBER: US/09/497,591
 CURRENT FILING DATE: 2000-02-03
 EARLIER APPLICATION NUMBER: 08/955,636
 EARLIER FILING DATE: 1999-04-19
 EARLIER APPLICATION NUMBER: 08/955,636
 EARLIER FILING DATE: 1997-10-23
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 44
 TYPE: PRT
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (0) ..(0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-497-591-3

Query Match Score 161.5; DB 4; Length 44;
 Best Local Similarity 97.8%; Pred. No. 1..le-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAVFLXXLRPGSLRXCXXQCSFXXXARXIFKDAVRTLFWI SY 45
 Db 1 ANA-FLXXLRPGSLRXCXXQCSFXXXARXIFKDAVRTLFWI SY 44

RESULT 4

US-09-803-810-3

Sequence 3, Application US/09803810
 Patent No. 6762386
 GENERAL INFORMATION:
 APPLICANT: Nelestuen, Gary L.
 TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
 TITLE OF INVENTION: POLYPEPTIDES
 FILE REFERENCE: 09511/002001
 CURRENT APPLICATION NUMBER: US/09/803,810
 CURRENT FILING DATE: 2001-03-12
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 44
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (0) ..(0)
 OTHER INFORMATION: xaa=gamma carboxyglutamic acid or glutamic acid

US-09-803-810-3

Query Match Score 161.5; DB 1; Length 406;
 Best Local Similarity 75.6%; Pred. No. 1..e-18;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAVFLXXLRPGSLRXCXXQCSFXXXARXIFKDAVRTLFWI SY 45
 Db 1 ANA-FLYTLRPGSLRYRKYTCQSFTARYIFKDAVRTLFWI SY 44

RESULT 6
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Masters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: For Inhibiting Coagulation

CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0., Version #1.25
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0., Version #1.25
NUMBER OF SEQUENCES: 10

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
INFORMATION FOR SEQ ID NO: 5:
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match Score 161.5; DB 2; Length 406;
Best Local Similarity 75.6%; Pred. No. 1e-18; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCXQCSFXARXIFKDAERTKLFWISY 45
Db 1 ANA-FDEELRPGSLERECQECSFEARIEFKDAERTKLFWISY 44

RESULT 7
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 568751
GENERAL INFORMATION:

RESULT 8
US-09-782-587B-1
Sequence 1, Application US/09782587B
Patent No. 6806063
GENERAL INFORMATION:
APPLICANT: PEDERSEN, ANDERS H.
APPLICANT: BORNHAUER, CLAUDIO
APPLICANT: BORNHAUER, CLAUDIO
TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
FILE REFERENCE: 31-001100US
CURRENT APPLICATION NUMBER: US/09/782,587B
CURRENT FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: PA 2000 00218
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 60/184,036
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/241,916
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 406
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MOD_RES
 LOCATION: (6) ..(7)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (14)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (16)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (19)..(20)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (25)..(26)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (29)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 NAME/KEY: MOD_RES
 LOCATION: (35)
 OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
 US-09-782-587B-1

Query Match Score 81.2%; Pred. No. 1e-18; Length 406;
 Best Local Similarity 97.8%; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCXXXQCSFXARXKIFKDAXRTKLFWIISY 45
 Db 1 ANA-FLXXLRPGSLXRXCXXXQCSFXARXKIFKDAXRTKLFWIISY 44

RESULT 9
 US-09-782-587B-3
 Sequence 3 Application US/09782587B
 Patent No. 6806063
 GENERAL INFORMATION:
 APPLICANT: PEDERSEN, ANDERS H.
 APPLICANT: ANDERSON, KIM V.
 APPLICANT: BORNNAES, CLAUS
 TITLE OF INVENTION: FACTOR VII OR VIA-LIKE MOLECULES
 FILE REFERENCE: 31-001100US
 CURRENT APPLICATION NUMBER: US/09/782,587B
 CURRENT FILING DATE: 2002-03-26
 PRIOR APPLICATION NUMBER: PA 2000 00218
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 60/184,036
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/241,916
 PRIOR FILING DATE: 2000-10-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3
 LENGTH: 406
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-782-587B-3

Query Match Score 81.2%; Pred. No. 1e-18; Length 406;
 Best Local Similarity 75.6%; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCXXXQCSFXARXKIFKDAXRTKLFWIISY 45
 Db 1 ANA-FLXXLRPGSLXRXCXXXQCSFXARXKIFKDAXRTKLFWIISY 44

RESULT 11
 US-08-475-845-2

Sequence 2, Application US/08475845
 GENERAL INFORMATION:
 APPLICANT: Berkner, Kathleen L.
 APPLICANT: Petersen, Lars C.
 APPLICANT: Hart, Charles E.
 APPLICANT: Hedner, Ulla
 APPLICANT: Bregenguard, Claus
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Stewart Street Tower
 CITY: San Francisco
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/327,690
 FILING DATE: 24-OCT-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/065,725
 FILING DATE: 21-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION NUMBER: 31,990
 REFERENCE/DOCKET NUMBER: 13952-8-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-467-9600
 TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-327-690-2

Query Match 91.2%; Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 1.1e-18;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAVFLXXLRPGSLRXCKXQCSFXKARIFDAERTKLFWISY 45
 Db 39 ANA-FLEELRPGSLERKEEQCSFEEARIFDAERTKLFWISY 82

RESULT 12
 US-08-327-690-2
 Sequence 2, Application US/08327690
 GENERAL INFORMATION:
 APPLICANT: Berkner, Kathleen L.
 APPLICANT: Petersen, Lars C.
 APPLICANT: Hart, Charles E.
 APPLICANT: Hedner, Ulla
 APPLICANT: Bregenguard, Claus
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Stewart Street Tower
 CITY: San Francisco
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/660-289
 FILING DATE:
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/475, 845
 FILING DATE: 21-MAY-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/327, 690
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/662, 920
 FILING DATE: 28-FEB-1991
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Parmelee, Steven W.
 REGISTRATION DOCKET NUMBER: 13952-8-4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-467-9600
 TELEFAX: 415-541-5043
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-660-289-2

Query Match 81.2%; Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 1..1e-18;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLXRCKXXQCSFXKARXIFKDAKRTKLFWISY 45
 Db 39 ANA-FLEERLRPGSLERCKEEOQSFEAREIFDAERTKLFWISY 82

RESULT 14
 US-08-537-807-2
 ; Sequence 2, Application US/08537807
 ; Patent No. 5861374
 GENERAL INFORMATION:
 APPLICANT: Modified Factor VII
 TITLE OF INVENTION: Modified Factor VII
 NUMBER OF SEQUENCES: 4
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/871,003
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Samislatk, Deborah A.
 REGISTRATION NUMBER: 37,438
 REFERENCE/DOCKET NUMBER: 90-07C7
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-871-003-2

Query Match 81.2%; Score 161.5; DB 2; Length 444;
 Best Local Similarity 75.6%; Pred. No. 1..1e-18;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLXRCKXXQCSFXKARXIFKDAKRTKLFWISY 45
 Db 39 ANA-FLEERLRPGSLERCKEEOQSFEAREIFDAERTKLFWISY 82

Search completed: August 22, 2005, 18:47:55
 Job time : 31 secs

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 22, 2005, 18:45:49 ; Search time 662 Seconds
(without alignments)

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Published Applications AA:
 1: /cgn2_6/ptodata/1/pubpa/us07_pubcomb.dep:*
 2: /cgn2_6/ptodata/1/pubpa/pct_new_pub.dep:*
 3: /cgn2_6/ptodata/1/pubpa/us06_new_pub.dep:*
 4: /cgn2_6/ptodata/1/pubpa/us06_pubcomb.dep:*
 5: /cgn2_6/ptodata/1/pubpa/us07_new_pub.dep:*
 6: /cgn2_6/ptodata/1/pubpa/pctus_pubcomb.dep:*
 7: /cgn2_6/ptodata/1/pubpa/us08_new_pub.dep:*
 8: /cgn2_6/ptodata/1/pubpa/us08_pubcomb.dep:*
 9: /cgn2_6/ptodata/1/pubpa/us09_pubcomb.dep:*
 10: /cgn2_6/ptodata/1/pubpa/us09_pubcomb.dep:*
 11: /cgn2_6/ptodata/1/pubpa/us09_pubcomb.dep:*
 12: /cgn2_6/ptodata/1/pubpa/us09_new_pub.dep:*
 13: /cgn2_6/ptodata/1/pubpa/us10_pubcomb.dep:*
 14: /cgn2_6/ptodata/1/pubpa/us10_pubcomb.dep:*
 15: /cgn2_6/ptodata/1/pubpa/us10_pubcomb.dep:*
 16: /cgn2_6/ptodata/1/pubpa/us10_pubcomb.dep:*
 17: /cgn2_6/ptodata/1/pubpa/us10_pubcomb.dep:*
 18: /cgn2_6/ptodata/1/pubpa/us10_new_pub.dep:*
 19: /cgn2_6/ptodata/1/pubpa/us11_pubcomb.dep:*
 20: /cgn2_6/ptodata/1/pubpa/us11_new_pub.dep:*
 21: /cgn2_6/ptodata/1/pubpa/us60_new_pub.dep:*
 22: /cgn2_6/ptodata/1/pubpa/us60_pubcomb.dep:*

RESULT 1
US-09-803-810-3
; Sequence 3, Application US/09803810
; Publication No. US20010018414A1
; GENERAL INFORMATION:
; APPLICANT: Neisseuen, Gary L.
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 0951/002001
; CURRENT APPLICATION NUMBER: US/09/803,810
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0) .. (0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid

Query Match 91.2%; Score 161.5; DB 9; Length 44;
Best Local Similarity 97.8%; Pred. No. 4.5e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAVFLXXIRPGLSLRXCXXQSPFXARXIFDAXTRKLFWISY 45
1 ANA FLXXIRPGLSLRXCXXQSPFXARXIFDAXTRKLFWISY 44
Db 1 ANA FLXXIRPGLSLRXCXXQSPFXARXIFDAXTRKLFWISY 44

RESULT 2
US-10-298-330-3

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	81.2	44	9 US-09-803-810-3	Sequence 3, Appli
2	161.5	81.2	44	14 US-10-298-330-3	Sequence 3, Appli
3	161.5	81.2	44	16 US-10-855-068-3	Sequence 3, Appli
4	161.5	81.2	406	10 US-09-782-587B-1	Sequence 1, Appli
5	161.5	81.2	406	10 US-09-782-587B-3	Sequence 3, Appli
6	161.5	81.2	406	14 US-10-109-498-1	Sequence 1, Appli
7	161.5	81.2	406	14 US-10-255-032-1	Sequence 1, Appli
8	161.5	81.2	406	14 US-10-281-727-1	Sequence 1, Appli
9	161.5	81.2	406	15 US-10-386-898-7	Sequence 7, Appli
10	161.5	81.2	406	15 US-10-383-898-1	Sequence 1, Appli
11	161.5	81.2	406	15 US-10-617-500-1	Sequence 1, Appli

Sequence 3, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsbeuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-3-30-3

Query Match 81.2%; Score 161.5; DB 14; Length 44;
Best Local Similarity 97.8%; Pred. No. 4.5e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAYFLXXLRPGSLXRXCXQXQCSXXKARXIFKDAKXTKLFWIISY 45
Qy 1 ANAYFLXXLRPGSLXRXCXQXQCSXXKARXIFKDAKXTKLFWIISY 44

RESULT 3
US-10-855-068-3
; Sequence 3, Application US/10855068
; Publication No. US20040220106A1
; GENERAL INFORMATION:
; APPLICANT: Nelsbeuen, Gary L.
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531-002001
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0) . . . (0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-10-855-068-3

Query Match 81.2%; Score 161.5; DB 16; Length 44;
Best Local Similarity 97.8%; Pred. No. 4.5e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAYFLXXLRPGSLXRXCXQXQCSXXKARXIFKDAKXTKLFWIISY 45
Qy 1 ANAYFLXXLRPGSLXRXCXQXQCSXXKARXIFKDAKXTKLFWIISY 44

RESULT 4
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Publication No. US20030096330A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAE, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; SOFTWARE: Patentin Ver. 2.1
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6) . . . (7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (19). . . (20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (25). . . (26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD_RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match 81.2%; Score 161.5; DB 10; Length 406;
Best Local Similarity 97.8%; Pred. No. 4.1e-19;
Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLXRXCXQXQCSXXKARXIFKDAKXTKLFWIISY 45
Db 1 ANA-FLXXLRPGSLXRXCXQCSXXKARXIFKDAKXTKLFWIISY 44

RESULT 5
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096330A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAE, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3 LENGTH: 406

TYPE: PRT ORGANISM: Homo sapiens

US-09-782-587B-3

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAYFLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 8 US-10-281-727-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Db 1 ANA-FLEBLRPGSLREKEFQCSPEEARIEFKDAERTKLFWISY 44

RESULT 6 US-10-109-498-1

Sequence 1, Application US/10109498

Publication No. US20030044908A1

GENERAL INFORMATION:

APPLICANT: Person, Egon

TITLE OF INVENTION: Coagulation Factor VII Derivatives

FILE REFERENCE: 6286_200.US

CURRENT APPLICATION NUMBER: US/10/109,498

PRIOR APPLICATION NUMBER: 2002-03-22

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: 60/281,261

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: PA 2001 00477

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 406

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: VARIANT

LOCATION: (1)...(406)

OTHER INFORMATION: Xaa = Any Amino Acid

US-10-109-498-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAYFLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 9 US-10-386-898-7

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 7 US-10-255-032-1

Sequence 1, Application US/10255032

Publication No. US20030100075A1

GENERAL INFORMATION:

APPLICANT: No. US20030100075A1 No. US20030100075A1

TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

FILE REFERENCE: 6357_WO

CURRENT APPLICATION NUMBER: US/10/255,032

PRIOR APPLICATION NUMBER: DK PA 2001 01413

PRIOR FILING DATE: 2001-09-27

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 406

TYPE: PRT

ORGANISM: human coagulation Factor VII

FEATURE: MISC_FEATURE

LOCATION: (1)...(406)

OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

US-10-255-032-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANAYFLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 8 US-10-281-727-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 9 US-10-386-898-7

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 7 US-10-255-032-1

Sequence 1, Application US/10255032

Publication No. US20030100075A1

GENERAL INFORMATION:

APPLICANT: No. US20030100075A1 No. US20030100075A1

TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

FILE REFERENCE: 6445_WO

CURRENT APPLICATION NUMBER: US/10/386,898

PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373

PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/365,935

PRIOR FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7

LENGTH: 406

TYPE: PRT

ORGANISM: human coagulation Factor VII

FEATURE: MISC_FEATURE

NAME/KEY: (1)...(406)

LOCATION: (1)...(406)

OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

US-10-255-032-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 8 US-10-281-727-1

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 9 US-10-386-898-7

Query Match Score 81.2%; Best Local Similarity 97.8%; Pred. No. 4.1e-19; Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 45

1 ANA-FLXXLRPGSLXRXCQXXQCSFXKARXIFKDAXRTKLFWISY 44

RESULT 7 US-10-255-032-1

Sequence 1, Application US/10255032

Publication No. US20030100075A1

GENERAL INFORMATION:

APPLICANT: No. US20030100075A1 No. US20030100075A1

TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES

FILE REFERENCE: 6445_WO

CURRENT APPLICATION NUMBER: US/10/386,898

PRIOR APPLICATION NUMBER: Danish Application PA 2002 00373

PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/365,935

PRIOR FILING DATE: 2002-03-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7

LENGTH: 406

TYPE: PRT

ORGANISM: human coagulation Factor VII

FEATURE: MISC_FEATURE

NAME/KEY: (1)...(406)

LOCATION: (1)...(406)

OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)

; OTHER INFORMATION: xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-386-898-7

Query Match Score 161.5; DB 15; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCXQCSXXARXIFKDAXRTKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCXQCSXXARXIFKDAXRTKLFWISY 44

RESULT 11
 US-10-617-500-1

Query Match Score 161.5; DB 15; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCXQCSXXARXIFKDAXRTKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCXQCSXXARXIFKDAXRTKLFWISY 44

RESULT 12
 US-10-263-205B-2

Sequence 2, Application US/10263205B
 Publication No. US20040007498A1

GENERAL INFORMATION:
 ; APPLICANT: BEKKNER, Kathleen L.
 ; PETERSEN, Lars
 ; HART, Charles E.
 ; APPLICANT: HEDNER, Ulla
 ; APPLICANT: BREGENGAARD, Claus
 ; TITLE OF INVENTION: MODIFIED FACTOR VII
 ; FILE REFERENCE: 13952N-B-5-1
 ; CURRENT APPLICATION NUMBER: US/10/263, 205B
 ; CURRENT FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: 081464, 029
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: 081327, 690
 ; PRIOR FILING DATE: 1994-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US94/05779
 ; PRIOR FILING DATE: 1994-05-23
 ; PRIOR APPLICATION NUMBER: 081065, 725
 ; PRIOR FILING DATE: 1993-05-21
 ; PRIOR APPLICATION NUMBER: PCT/US92/01636
 ; PRIOR FILING DATE: 1991-02-28
 ; PRIOR APPLICATION NUMBER: 071662, 920
 ; PRIOR FILING DATE: 1991-02-28
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CHAIN
 ; LOCATION: (1) .. (406)

US-10-383-898-1

Query Match Score 161.5; DB 15; Length 406;
 Best Local Similarity 75.6%; Pred. No. 4.1e-19;
 Matches 34; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Qy 1 ANAYFLXXLRPGSLRXCXQCSXXARXIFKDAXRTKLFWISY 45
 Db 1 ANA-FLEELRPGSLERECKESEQSPEAREIFDAERIKLFWISY 44

RESULT 13
 US-10-617-619-1

Sequence 1, Application US/10617619
 Publication No. US20040072755A1

GENERAL INFORMATION:
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 ; APPLICANT: Stennicke, Henning R
 ; APPLICANT: Bjorn, Soren E
 ; APPLICANT: Petersen, Lars C
 ; TITLE OF INVENTION: TF Antagonist
 ; FILE REFERENCE: 6510-200-US
 ; CURRENT APPLICATION NUMBER: US/10/617, 500
 ; CURRENT FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01100
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: US 60/404, 567
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 406
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; OTHER INFORMATION: Synthetic
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (1) .. (406)
 ; OTHER INFORMATION: xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 ; US-10-617-500-1

RESULT 14
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Synthetic
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (1) .(406)
 OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-617-619-1
 Query Match 81.2%; Score 161.5; DB 16; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXCKXXQCSFXXARXIFKDAKRTRKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCKXXQCSFXXARXIFKDAKRTRKLFWISY 44
 RESULT 14
 Sequence 1, Application US/10701294
 Publication No. US2004014309A1
 GENERAL INFORMATION:
 APPLICANT: Novo Nordisk Pharmaceuticals, Inc.
 APPLICANT: Petersen, Lars C
 APPLICANT: Back, Jacob M
 APPLICANT: Meyer, Christian
 TITLE OF INVENTION: Pharmaceutical Composition Comprising a Tissue Factor Antagonist
 FILE REFERENCE: 6608-200-US
 CURRENT APPLICATION NUMBER: US/10/701,294
 CURRENT FILING DATE: 2003-11-04
 PRIOR APPLICATION NUMBER: US 60/434,904
 PRIOR FILING DATE: 2002-12-20
 PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01710
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 1
 LENGTH: 406
 TYPE: PRT
 ORGANISM: human coagulation Factor VII
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (1) .(406)
 OTHER INFORMATION: Xaa=4-carboxyglutamic acid (gamma-carboxyglutamate)
 US-10-701-294-1
 Query Match 81.2%; Score 161.5; DB 16; Length 406;
 Best Local Similarity 97.8%; Pred. No. 4.1e-19;
 Matches 44; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 ANAYFLXXLRPGSLRXCKXXQCSFXXARXIFKDAKRTRKLFWISY 45
 Db 1 ANA-FLXXLRPGSLRXCKXXQCSFXXARXIFKDAKRTRKLFWISY 44
 RESULT 15
 US-10-669-537-1
 Sequence 1, Application US/10669537
 Publication No. US2005019260A1
 GENERAL INFORMATION:
 APPLICANT: Persson, Egon
 APPLICANT: Olsen, Ole Hvilsted
 TITLE OF INVENTION: Human Coagulation Factor VII Polypeptides
 FILE REFERENCE: 6544-200-US
 CURRENT APPLICATION NUMBER: US/10/669,537
 CURRENT FILING DATE: 2003-09-24
 PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01423
 PRIOR FILING DATE: 2002-09-25
 PRIOR APPLICATION NUMBER: US 60/417,927
 PRIOR FILING DATE: 2002-10-11
 NUMBER OF SEQ ID NOS: 13

This Page Blank (uspto)